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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 98.2%; Score 1230; DB 9; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 1230; Conservative 0;
QY 24 GCGAGGCGAGAGCCCGCTTCGCTAGCGGCTGCTCAGAGTGTGTCTCTGCTCGC 83
DB 1 GCGAGGCGAGAGCCCGCTTCGCTAGCGGCTGCTCAGAGTGTGTCTCTGCTCGC 60
QY 84 CTCAGATGAGGAGGAGATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGAGCTTCTGTC 143
DB 61 CTCAGATGAGGAGGAGATCTGGCCCTGGTGGGCGTTCTAATCAGCCTTCTGTC 120
QY 144 CTGCTGCGATCTGACATCTTCAGCCGCTGGCGATGACGCTGCTCTGTGCAATCTTC 203
DB 121 CTGCTGCGATCTGACATCTTCAGCCGCTGGCGATGACGCTGCTCTGTGCAATCTTC 180
QY 204 GTCCCTGGCTTCAAGGGGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGCT 263
DB 181 GTCCCTGGCTTCAAGGGGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGCT 240
QY 264 GGAAGAGTCGCGCCCGCAGGAGAGAAAGAGCATGCGGAGCAAAAGGAGCAGAAAGGAGT 323
DB 241 GGAAGAGTCGCGCCCGCAGGAGAGAAAGAGCATGCGGAGCAAAAGGAGCAGT 300
QY 324 GTGGTCTCTCATGAGAAATTTGCTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGT 383
DB 301 GTGGTCTCTCATGAGAAATTTGCTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGT 360
QY 384 GACATAGACCCCTGCTCTCTAATGAGAAACAGGCTTCCATGTGAGTGCAGCCAGCTG 443
DB 361 GACATAGACCCCTGCTCTCTAATGAGAAACAGGCTTCCATGTGAGTGCAGCCAGCTG 420
QY 444 CGCAAGGCGCATCGGAGAGATGAGCAACAGGCTCTCAGCTGACCAAGGAGCTCAAGTTC 503
DB 421 CGCAAGGCGCATCGGAGAGATGAGCAACAGGCTCTCAGCTGACCAAGGAGCTCAAGTTC 480
QY 504 ATCAAGAAATGCTGTGCTGCTGTGTGCGAGAGCAGAGCAAGATTAATCTGTGTGAAG 563
DB 481 ATCAAGAAATGCTGTGCTGCTGTGTGCGAGAGCAGAGATTAATCTGTGTGAAG 540
QY 564 GAGAGAAAGCGCTTACGCGAGCGCCCAAGCTGTCTTCTGCGAGGCGCGGGGGGAGCTGAGC 623
DB 541 GAGAGAAAGCGCTTACGCGAGCGCCCAAGCTGTCTTCTGCGAGGCGCGGGGGGAGCTGAGC 600
QY 624 ATGCCCAAGAGAGAGGCTGCGCAATGAGGCTGATGCGGATATCTGCGCAAGCGGCGCTG 683
DB 601 ATGCCCAAGAGAGAGGCTGCGCAATGAGGCTGATGCGGATATCTGCGCAAGCGGCGCTG 660
QY 684 GCCCGTGTCTTCTCATGCGGATCAACAGCTGAGAGAGAGGCGCTTCTGTACTCTGAC 743
DB 661 GCCCGTGTCTTCTCATGCGGATCAACAGCTGAGAGAGAGGCGCTTCTGTACTCTGAC 720

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QY 744 CACTCCCCCATGCGGAGCCTTCAACAGTGGGAGCGGCTGAGCCCAACATGCTTACGAC 803
DB 721 CACTCCCCCATGCGGAGCCTTCAACAGTGGGAGCGGCTGAGCCCAACATGCTTACGAC 780
QY 804 GAGAGAGACTGCTGAGAGTGTGCTCGGCGGCTGGAAGAGAGTGGCTGCGACAGC 863
DB 781 GAGAGAGACTGCTGAGAGTGTGCTCGGCGGCTGGAAGAGAGTGGCTGCGACAGC 840
QY 864 ACCATGTACTTCAATGTGTGAGTGTGACAGAGAAACATGTGAGCTTCAAGCTGAGGCTG 923
DB 841 ACCATGTACTTCAATGTGTGAGTGTGACAGAGAAACATGTGAGCTTCAAGCTGAGGCTG 900
QY 924 CCATTGGGGGGCCCAACATGCTTCCGAGGAGTGGAGGAGAGAGCCCAACATGCTG 983
DB 901 CCATTGGGGGGCCCAACATGCTTCCGAGGAGTGGAGGAGAGAGCCCAACATGCTG 960
QY 984 CAGCAGGAGAGCTGTCTCTGTGAGAGGAGGAGCTCACTGAGTGAAGGCTGTGTCT 1043
DB 961 CAGCAGGAGAGCTGTCTCTGTGAGAGGAGGAGCTCACTGAGTGAAGGCTGTGTCT 1020
QY 1044 AAATGAGAAATGAGCTTATGAGAGAAATGAAAGTGTCTGAGGCTGTGTCT 1103
DB 1021 AAATGAGAAATGAGCTTATGAGAGAAATGAAAGTGTCTGAGGCTGTGTCT 1080
QY 1104 TGAAGAGCAGAGTTTCAATTAACCTGTATTTGAGCCCAATGCAATTAATTAATTAAC 1163
DB 1081 TGAAGAGCAGAGTTTCAATTAACCTGTATTTGAGCCCAATGCAATTAATTAATTAAC 1140
QY 1164 CAGAAATGCTTCTTCAATTAAGCTGTGCTTGTGCAAGTATACATTAATCTTTAAG 1223
DB 1141 CAGAAATGCTTCTTCAATTAAGCTGTGCTTGTGCAAGTATACATTAATCTTTAAG 1200
QY 1224 TAGTGCACTAGTTAAGTCAAAAAAAA 1253
DB 1201 TAGTGCACTAGTTAAGTCAAAAAAAA 1230

RESULT 2
US-09-989-723-356
; Sequence 356, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ealson, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zenlin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989, 723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787

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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Beet Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GCGAGGCGAGAGCCCGCTTGGCGCTTATAGCGCTGCTCAGAGTGGTGTCTCTGCTGCG 83  
Db 1 GCGAGGCGAGAGCCCGCTTGGCGCTTATAGCGCTGCTCAGAGTGGTGTCTCTGCTGCG 60  
Qy 84 CTGAGATGAGGAGGAGATCTGGCCGCGGCTTCTATAGCGCTGCTCAGAGTGGTGTCTCTGCTGCA 143  
Db 61 CTCAGATGAGGAGGAGATCTGGCCGCGGCTTCTATAGCGCTGCTCAGAGTGGTGTCTCTGCTGCA 120  
Qy 144 CTGCTGCAATCTGAGCATCTCTGAGCGCGCTGCGATGAGCGCTGCTCTGTGCAATCTCTC 203  
Db 121 CTGCTGCAATCTGAGCATCTCTGAGCGCGCTGCGATGAGCGCTGCTCTGTGCAATCTCTC 180  
Qy 204 GTCCCTGGCTTAAAGGGAGATCGGGAGAGAAAGGAGCAAAAGGCGCCCGCGAGCGCT 263  
Db 181 GTCCCTGGCTTAAAGGGAGATCGGGAGAGAAAGGAGCAAAAGGCGCCCGCGAGCGCT 240  
Qy 264 GGAAGATCGGCGCCCGAG 323  
Db 241 GGAAGATCGGCGCCCGAG 300  
Qy 324 GTGGCTGCTATGAGAAATTTGGTCCATTTGCTCTAAAGGTGAGAAAGAGAGATTCGGT 383  
Db 301 GTGGCTGCTATGAGAAATTTGGTCCATTTGCTCTAAAGGTGAGAAAGAGAGATTCGGT 360  
Qy 384 GACATAG 443  
Db 361 GACATAG 420  
Qy 444 GCGAG 503  
Db 421 GCGAG 480  
Qy 504 ATCAAGATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
Db 481 ATCAAGATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Qy 564 GAG 623  
Db 541 GAG 600  
Qy 624 ATGCCAAG 683  
Db 601 ATGCCAAG 660  
Qy 684 GCCCGTGTCTTATCGGAGATCAAG 743  
Db 661 GCCCGTGTCTTATCGGAGATCAAG 720

Qy 744 CACTCCCCATGCGGAGAGCTTCAACAAGTGGGAGAGCGGTGAGCCCAACATGCTTACAGAC 803  
Db 721 CACTCCCCATGCGGAGAGCTTCAACAAGTGGGAGAGCGGTGAGCCCAACATGCTTACAGAC 780  
Qy 804 GAG 863  
Db 781 GAG 840  
Qy 864 ACCATGTAATCTGATGAG 923  
Db 841 ACCATGTAATCTGATGAG 900  
Qy 924 CCATTTGGGGGCGCCCAATGCTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
Db 901 CCATTTGGGGGCGCCCAATGCTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
Qy 984 CAGCCAG 1043  
Db 961 CAGCCAG 1020  
Qy 1044 AAATGAG 1103  
Db 1021 AAATGAG 1080  
Qy 1104 TGAAG 1163  
Db 1081 TGAAG 1140  
Qy 1164 CAGAAATGCTCTTCAATGAG 1223  
Db 1141 CAGAAATGCTCTTCAATGAG 1200  
Qy 1224 TAGTGCAGTAAAGTCAAAAAA 1253  
Db 1201 TAGTGCAGTAAAGTCAAAAAA 1230

RESULT 3  
US-09-989-279-356  
Sequence 356, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acid Encoding the Same  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989, 279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787



PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGACGGGACAGAGCCCGCTTCCGCTAGCGGCTCTCAAGAGTTGTCTCTGCTCGC 83  
DB 1 GCGACGGGACAGAGCCCGCTTCCGCTAGCGGCTCTCAAGAGTTGTCTCTGCTCGC 60  
QY 84 CTCAGATGAGGGGAGATCTGGCCCTGGGGGCTTCTAATACGCTGAGCTTCTCTCA 143  
DB 61 CTCAGATGAGGGGAGATCTGGCCCTGGGGGCTTCTAATACGCTGAGCTTCTCTCA 120  
QY 144 CTGCTGCATCTGACATCTCAAGCGGCTGGCGATGACGCGTCTCTGTGCAATCTTC 203  
DB 121 CTGCTGCATCTGACATCTCAAGCGGCTGGCGATGACGCGTCTCTGTGCAATCTTC 180  
QY 204 GTCCCTGGCTTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGGCTTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTGGGCGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTGGGCGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGCTCTCAATGAAAAATGGTCCATTTGGCTCTAAGGTGAGAAAGAGATTCCGGT 383  
DB 301 GTGGCTCTCAATGAAAAATGGTCCATTTGGCTCTAAGGTGAGAAAGAGATTCCGGT 360  
QY 384 GACATGAGACCCCTGGTCTCTAATGAGAACAGGCTTCCATTTGAGTGCAGCCAGCTG 443  
DB 361 GACATGAGACCCCTGGTCTCTAATGAGAACAGGCTTCCATTTGAGTGCAGCCAGCTG 420  
QY 444 CGCAAGGCTATCGGGAGATGAGAACAGGCTCTCAAGCTGACCAAGGAGGCTCAAGTTC 503  
DB 421 CGCAAGGCTATCGGGAGATGAGAACAGGCTCTCAAGCTGACCAAGGAGGCTCAAGTTC 480  
QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGATCTACCTGTGTGAAG 563  
DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGATCTACCTGTGTGAAG 540  
QY 564 GAGAGAAAGCGCTACGCGAGAGCGCCAGCTGTCTCCAGGCGCGCGGGGAGACGCTGAGC 623  
DB 541 GAGAGAAAGCGCTACGCGAGAGCGCCAGCTGTCTCCAGGCGCGCGGGGAGACGCTGAGC 600  
QY 624 ATGCCCAAG 683  
DB 601 ATGCCCAAG 660  
QY 684 GCCCGTCTTCTATCGGATCAACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGTCTTCTATCGGATCAACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCATGGGAGACTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803  
DB 721 CACTCCCCATGGGAGACTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
QY 804 GAG 863  
DB 781 GAG 840  
QY 864 ACCATGTAATCTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
DB 841 ACCATGTAATCTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 924 CCATTTGGGGGCGCCCAATGTCCTCGAGGGGTTGGCAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTTGGGGGCGCCCAATGTCCTCGAGGGGTTGGCAGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCAG 1043  
DB 961 CAGCAG 1020  
QY 1044 AAAGTGAAGAAATGAGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103  
DB 1021 AAAGTGAAGAAATGAGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
QY 1104 TGAAG 1163  
DB 1081 TGAAG 1140  
QY 1164 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCAAGAGTATCAATTAATCTTTAAG 1223  
DB 1141 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCAAGAGTATCAATTAATCTTTAAG 1200  
QY 1224 TAGTGAGTAAAGTCAAAAAA 1253  
DB 1201 TAGTGAGTAAAGTCAAAAAA 1230

RESULT 4  
US-09-989-727-356  
Sequence 356, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deemoyers, Luc  
APPLICANT: Falcon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Pan, James  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C65  
CURRENT APPLICATION NUMBER: US/09/989, 727  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

1 PRIOR FILING DATE: 1998-06-26  
 2 PRIOR APPLICATION NUMBER: 60/090863  
 3 PRIOR FILING DATE: 1998-06-26  
 4 PRIOR APPLICATION NUMBER: 60/091360  
 5 PRIOR FILING DATE: 1998-07-01  
 6 PRIOR APPLICATION NUMBER: 60/091478  
 7 PRIOR FILING DATE: 1998-07-02  
 8 PRIOR APPLICATION NUMBER: 60/091544  
 9 PRIOR FILING DATE: 1998-07-01  
 10 PRIOR APPLICATION NUMBER: 60/091519  
 11 PRIOR FILING DATE: 1998-07-02  
 12 PRIOR APPLICATION NUMBER: 60/091626  
 13 PRIOR FILING DATE: 1998-07-02  
 14 PRIOR APPLICATION NUMBER: 60/091633  
 15 PRIOR FILING DATE: 1998-07-02  
 16 PRIOR APPLICATION NUMBER: 60/091978  
 17 PRIOR FILING DATE: 1998-07-07  
 18 PRIOR APPLICATION NUMBER: 60/091982  
 19 PRIOR FILING DATE: 1998-07-07  
 20 PRIOR APPLICATION NUMBER: 60/092182  
 21 PRIOR FILING DATE: 1998-07-09

Query Match	98.2%	Score 1230;	DB 9;	Length 1238;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1230; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	24	GGGAGCGGGGAGGACGCGCCGGTTCGACTTAGCGCGTGCCTCAGAAATTGATGTCTCGCCAGCG	83
Db	1	GGGAGCGGGGAGGACGCGCCGGTTCGACTTAGCGCGTGCCTCAGAAATTGATGTCTCGCCAGCG	60
OY	84	CTCAGGATGAGGGGGGAATCTGGCCCTGTGGGGCGTTCTAATCAGCCCTGGCTTCTGTCA	143
Db	61	CTCAGGATGAGGGGGGAATCTGGCCCTGTGGGGCGTTCTAATCAGCCCTGGCTTCTGTCA	120
OY	144	CTGCGTGCATCTGGACATCTCAGCGCGGCTGGGGATGAGCGCGCTGTGGCAGATCTTC	203
Db	121	CTGCTTGCATCTGGACATCTCAGCGCGGCTGGGGATGAGCGCTGTGTGTGGCAATCTTC	180
OY	204	GTCCTTGCCCTTCAAAAGGGGATGGGGGAGAAAGGAGACAAAGCGCCCCCGGACGGCCT	263
Db	181	GTCCTTGCCCTTCAAAAGGGGATGGGGGAGAAAGGAGACAAAGCGCCCCCGGACGGCCT	240
OY	264	GGAAGAGTGGGCCCCACGGGAGAAAAGAGACATGGGGGCAAAAGACAGAAAGGCAT	323
Db	241	GGAAGAGTGGGCCCCACGGGAGAAAAGAGACATGGGGGCAAAAGACAGAAAGGCAT	300
OY	324	GTCGGTCCGTCATGGAAAAATTGGTCCATTGGCTCTAAAGGTAGAAAGGAGATTCCGCT	383
Db	301	GTCGGTCCGTCATGGAAAAATTGGTCCATTGGCTCTAAAGGTAGAAAGGAGATTCCGCT	360
OY	384	GACATAGGACCCCCCTGTGTCCTAATGGAGAACCAAGGCTTCCATGTGATGTGCACGCAGCTG	443
Db	361	GACATAGGACCCCCCTGTGTCCTAATGGAGAACCAAGGCTTCCATGTGATGTGCACGCAGCTG	420
OY	444	CGCAAGGCCCATCGGGGAGATGGACAACCAAGGTCCTCAGCTGACCAAGCGAGCTCAAGTTC	503
Db	421	CGCAAGGCCCATCGGGGAGATGGACAACCAAGGTCCTCAGCTGACCAAGCGAGCTCAAGTTC	480
OY	504	ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGACGGAGAGCAAAATCTAATCTGTGTGAAG	563
Db	481	ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGACGGAGAGCAAAATCTAATCTGTGTGAAG	540
OY	564	GAGGAGGAAGCGCTTACGCGGACGCGCCAGCTGTCTGTCAAGGCGCGGGGGGCAAGCTGAGC	623
Db	541	GAGGAGGAAGCGCTTACGCGGACGCGCCAGCTGTCTGTGTCAAGGCGCGGGGGGCAAGCTGAGC	600
OY	624	ATGCCCAAGACGAGGCTGCATATGGCTGTATGGCCGATACCTTGGCGCAAGCGGCGCTG	683
Db	601	ATGCCCAAGACGAGGCTGCATATGGCTGTATGGCCGATACCTTGGCGCAAGCGGCGCTG	660
OY	684	GCCCCGTGTTTCAATCGGCATCAACGACTGGAGAAAGAGGGCGCCTTCGTGTACTCTGAC	743
Db	661	GCCCCGTGTTTCAATCGGCATCAACGACTGGAGAAAGAGGGCGCCTTCGTGTACTCTGAC	720

QY	144	AACTCCCCAAGGGAGACCTTCAACAAGGGGCGACGGGTGAGCCCAACATAGCTTAGAC	803
Db	721	CATCCCCCAATGGCGAACCTTCAACAAGTGGCGCACGGGTGAGCCCAACATAGCTTAGAC	780
QY	804	GAGAGGAGCTGCTGTGAGATGTGTGGCTCGGGCGGCTGGAACGACGTGGCTGGCAACC	863
Db	781	GAGAGGAGCTGCTGTGAGATGTGTGGCTCGGGCGGCTGGAACGACGTGGCTGGCAACC	840
QY	864	ACCATGTACTTCATGTGTGAATTTGACAGAGAACATGTGAGCTTCAAGCTTGGGGCTGC	923
Db	841	ACCATGTACTTCATGTGTGAATTTGACAGAGAACATGTGAGCTTCAAGCTTGGGGCTGC	900
QY	924	CCATTGGGGGGCCCCACATGTCTCCGTGACAGGGTTGGCAGAGGACAGAGCCCAACATGTGTC	983
Db	901	CCATTGGGGGGCCCCACATGTCTCCGTGACAGGGTTGGCAGAGGACAGAGCCCAACATGTGTC	960
QY	984	CAGCCAGGGAGCTGTCCCTCTGTGTAAGGGGTGAGAGCTCACTGAGTAGAGGCTGTGTCT	1043
Db	961	CAGCCAGGGAGCTGTCCCTCTGTGTAAGGGGTGAGAGCTCACTGAGTAGAGGCTGTGTCT	1020
QY	1044	AAACTGAGAAATGGCCTATGCTTAAAGAGAAATGAAAGTTCCTGGGGTGTGCTCTC	1103
Db	1021	AAACTGAGAAATGGCCTATGCTTAAAGAGAAATGAAAGTTCCTGGGGTGTGCTCTC	1080
QY	1104	TGAAGAACAGAGTTCTATTACTGTATTTGATGTAGCCCAATGTCATTATGTAATATTACC	1163
Db	1081	TGAAGAACAGAGTTCTATTACTGTATTTGATGTAGCCCAATGTCATTATGTAATATTACC	1140
QY	1164	CAGAAATGCTCTTCCATTAAGCTTGTGCTTTGTCCAGACTATCAATTAATCTTTAAG	1223
Db	1141	CAGAAATGCTCTTCCATTAAGCTTGTGCTTTGTCCAGACTATCAATTAATCTTTAAG	1200
QY	1224	TAGTGCAGTAGTTAAGTCCAAAAAATAA 1253	
Db	1201	TAGTGCAGTAGTTAAGTCCAAAAAATAA 1230	

RESULT 5  
US-09-989-731-356  
Sequence 356, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsels, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P27301C170  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR APPLICATION NUMBER: 60/091633  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGACGGGAGAGACCCCGCTTCCCTTACGCGCTGCTCAGAGTTGTGTCTGCTGCG 83  
DB 1 GCGACGGGAGAGACCCCGCTTCCCTTACGCGCTGCTCAGAGTTGTGTCTGCTGCG 60  
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DB 61 CTCAGATGAGGGGGAATCTGGCCCTGGGGGCTTCTTAATAGCTGGCCCTCTCTGCA 120  
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DB 121 CTGCTGCAATCTGACATCTCTCAGCGCGCTGCGATGACGCTGCTGCTGCGATCTTC 180  
QY 204 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGGCGCCCGGACGCGCT 263  
DB 181 GTCCCTGGCTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGGCGCCCGGACGCGCT 240  
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DB 361 GACATAGACCCCGCTGCTTAAATGAGAAACAGGCTTCCATGTGAGTCAGCGACGTG 420  
QY 444 CGCAAGGCTATCGGGAGATGAGCAACAGGTCTCTCAAGCTGACCAAGAGGTCAAGTTC 503  
DB 421 CGCAAGGCTATCGGGAGATGAGCAACAGGTCTCTCAAGCTGACCAAGAGGTCAAGTTC 480  
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; Sequence 356, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deemoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltzen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C57  
; CURRENT APPLICATION NUMBER: US/09/989,732  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787

[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 GCGACGGGAGAGAGCGCCGCTTACGCGCTGCTCAGAGTTGCTGCTGCG 83  
1 GCGACGGGAGAGAGCGCCGCTTACGCGCTGCTCAGAGTTGCTGCTGCG 60  
84 CTGAG 143  
61 CTGAG 120  
144 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203  
121 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
204 GTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263  
181 GTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
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481 ATCAAG 540  
564 GAG 623  
541 GAG 600  
624 ATGCGAG 683  
601 ATGCGAG 660  
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661 GCGCGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

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1201 TAGTGCAGT 1230

RESULT 7  
US-09-991-073-356  
Sequence 356, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Auecin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

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PRIOR FILING DATE:	1998-06-12

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QY 24 GCGACGGGACAGACGCCCCCTTCCGCTGAGCGGCTCTCAGAGATTGGTCTCTGCTCGG 83  
DB 1 GCGACGGGACAGACGCCCCCTTCCGCTGAGCGGCTCTCAGAGATTGGTCTCTGCTCGG 60  
QY 84 CTCAGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTATCAGCCCTGAGCCCTCTGCA 143  
DB 61 CTCAGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTATCAGCCCTCTGCA 120  
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QY 204 GTCCCTGCTCTCAAAAGGGGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGGCT 263  
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QY 1224 TAGTCAAGTAAAGTCAAAAAAAA 1253  
DB 1201 TAGTCAAGTAAAGTCAAAAAAAA 1230

RESULT 9  
US-09-991-163-356  
Sequence 356, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Ealson, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C17  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

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2	PRIOR FILING DATE: 1998-06-16
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4	PRIOR FILING DATE: 1998-06-16
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26	PRIOR FILING DATE: 1998-06-19
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69	PRIOR APPLICATION NUMBER: 60/090662



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 ? PRIOR APPLICATION NUMBER: 60/091978  
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 ? PRIOR FILING DATE: 1998-07-07  
 ? PRIOR APPLICATION NUMBER: 60/092182  
 ? PRIOR FILING DATE: 1998-07-09

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Db	1	GCAGACGGACAGGACGCCCCGTTGCGCTTAGCGCGGTCTCAGAGATTGATCTCTCTGCTCGG	60		
QY	84	CTCAGAGATGAGGGGGAAATCTGGCCCTTGTTGGCGCTTCTAATCAGCCTGGCCTTCTGTCA	143		
Db	61	CTCAGAGATGAGGGGGAAATCTGGCCCTTGTTGGCGCTTCTAATCAGCCTGGCCTTCTGTCA	120		
QY	144	CTGCGGCCATGCGGACATCCTCAGCGCGGTGGCGGATGACCGCTGCTGTGTGAGATTCCTC	203		
Db	121	CTGCTGCCATCTGGACATCTTAGCGCGGTGGCGGATGACCGCTGCTGTGTGAGATTCCTC	180		
QY	204	GTCCTCTGGCTCTCAAGGGGATGCGGGAGAGAAAGGAGACAAGAGCGCCCCCGGACGGCTT	263		
Db	181	GTCCTCTGGCTCTCAAGGGGATGCGGGAGAGAAAGGAGACAAGAGCGCCCCCGGACGGCTT	240		
QY	264	GGAAGAGTGGGCCCCACGGGAGAAAAAGAGACATGGGGGACAAAGACAGAAAGGCACT	323		
Db	241	GGAAGAGTGGGCCCCACGGGAGAAAAAGAGACATGGGGGACAAAGACAGAAAGGCACT	300		
QY	324	GTTGGTGTCTCATGTGAAAAATTGGTCCCATTTGGCTCTTAAAGTGAAGAAAGAGATTCCGCT	383		
Db	301	GTTGGTGTCTCATGTGAAAAATTGGTCCCATTTGGCTCTTAAAGTGAAGAAAGAGATTCCGCT	360		
QY	384	GACATTAGGACCCCTGTGCTTAATAGAGAACCAAGGCTCCCATGTGAGTGCAGCCGACCTG	443		
Db	361	GACATTAGGACCCCTGTGCTTAATAGAGAACCAAGGCTCCCATGTGAGTGCAGCCGACCTG	420		
QY	444	CGCAAGGCTATCGGGGAGATGAGCAACAGGTTCTCTCAGCTGACCAAGCGAGCTCAAGTTT	503		
Db	421	CGCAAGGCTATCGGGGAGATGAGCAACAGGTTCTCTCAGCTGACCAAGCGAGCTCAAGTTT	480		
QY	504	ATCAAGAAATGCTGTTCGCCGCTGTGGCGGACGAGACGAGACAAATTTACTCTGTGGTGAAG	563		
Db	481	ATCAAGAAATGCTGTTCGCCGCTGTGGCGGACGAGACGAGACAAATTTACTCTGTGGTGAAG	540		
QY	564	GAGAGAAAGCCTACGCGGACGCGCAGCTGTCTCTCAGAGGCGCGGGGGGACAGCTGAGC	623		
Db	541	GAGAGAAAGCCTACGCGGACGCGCAGCTGTCTCTCAGAGGCGCGGGGGGACAGCTGAGC	600		
QY	624	ATGCCCAAGACGAGGCTGCCAATGAGCTGATGAGCCGACATACCTTGCGCAAGCCGAGCTTG	683		
Db	601	ATGCCCAAGACGAGGCTGCCAATGAGCTGATGAGCCGACATACCTTGCGCAAGCCGAGCTTG	660		
QY	684	GCCGCTGTCTTCAATCGGATCAACGACTTGAGAGAAAGAGGGGCTTTCGTGTACTCTGAC	743		
Db	661	GCCGCTGTCTTCAATCGGATCAACGACTTGAGAGAAAGAGGGGCTTTCGTGTACTCTGAC	720		

QY	744	CAC	CCCCC	CAAGGGG	CAAGGGG	CGCGGTG	AGCCCA	CAATG	CCCTAG	AG	803
Db	721	CAC	TCCCC	CAAGCGA	CTTCA	CAAGTGG	CGCGGTG	AGCCCA	CAATG	CCCTAG	803
QY	804	GAG	AGG	CACTG	CGG	AGATG	TGTGG	CGCTCG	GGAA	CGA	863
Db	781	GAG	AGG	CACTG	CGG	AGATG	TGTGG	CGCTCG	GGAA	CGA	863
QY	864	ACC	ATG	TCTT	CAATG	TGTGA	TTTGA	CAAGG	AACTG	TGAG	923
Db	841	ACC	ATG	TCTT	CAATG	TGTGA	TTTGA	CAAGG	AACTG	TGAG	923
QY	924	CC	ATTGG	GGGG	GGCC	CAATG	TCCCTG	GAAGG	GTGG	CAAGG	983
Db	901	CC	ATTGG	GGGG	GGCC	CAATG	TCCCTG	GAAGG	GTGG	CAAGG	983
QY	984	CAG	CCAGG	AGCTG	TCCCTG	TGTGA	AGG	GTGG	AGG	CTC	1043
Db	961	CAG	CCAGG	AGCTG	TCCCTG	TGTGA	AGG	GTGG	AGG	CTC	1043
QY	1044	AA	ACTG	AAAA	ATG	GCTT	CTTA	TGA	AG	AAAA	1103
Db	1021	AA	ACTG	AAAA	ATG	GCTT	CTTA	TGA	AG	AAAA	1103
QY	1104	TGA	AG	AG	CAG	TTTCA	TTC	TGTA	TG	TG	1163
Db	1081	TGA	AG	AG	CAG	TTTCA	TTC	TGTA	TG	TG	1163
QY	1164	CAG	ATG	TCTT	CCAT	TAA	AG	CTT	GTG	CTT	1223
Db	1141	CAG	ATG	TCTT	CCAT	TAA	AG	CTT	GTG	CTT	1223
QY	1224	TAG	TG	CAG	TAG	TAG	TCA	AAAA	AAAA	AAAA	1253
Db	1201	TAG	TG	CAG	TAG	TAG	TCA	AAAA	AAAA	AAAA	1253

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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 84 CTCAGATGAGGGGGAATCTGGCCCTGTGGGCGTTCTAATCAGCCTGAGCTTCTCTGCA 143  
DB 61 CTCAGATGAGGGGGAATCTGGCCCTGTGGGCGTTCTAATCAGCCTGAGCTTCTCTGCA 120  
QY 144 CTGCTGCATCTGACATCTTCAGCCGCTGCGATGACGCTTCTGTGCAATCTCTC 203  
DB 121 CTGCTGCATCTGACATCTTCAGCCGCTGCGATGACGCTTCTGTGCAATCTCTC 180  
QY 204 GTCCCTGGCTTCAAGGGGATCCGGGAGAGAAAGGCGCCCGCGAGAGGCT 263  
DB 181 GTCCCTGGCTTCAAGGGGATCCGGGAGAGAAAGGCGCCCGCGAGAGGCT 240  
QY 264 GGAAGAGTCGCGCCCGACGAGAGAAAGAGACATGGGGGACAAAGAGACAGAAAGCAGT 323  
DB 241 GGAAGAGTCGCGCCCGACGAGAGAAAGAGACATGGGGGACAAAGAGACAGAAAGCAGT 300  
QY 324 GTGGGTCTCATGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCCGAT 383  
DB 301 GTGGGTCTCATGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCCGAT 360  
QY 384 GACATAGAGACCCCTGTGTCTTATGAGAAACAGGCTTCCATGTGATGACAGCCAGCTG 443  
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QY 444 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTTCTCAGCTGACAGAGAGGTCAAGTTC 503  
DB 421 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTTCTCAGCTGACAGAGAGGTCAAGTTC 480  
QY 504 ATCAAGAAATGTGTGCGCGGTGTGCGAGACGAGAGACAGATTAATCTGTGTGAAG 563  
DB 481 ATCAAGAAATGTGTGCGCGGTGTGCGAGACGAGAGACAGATTAATCTGTGTGAAG 540  
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QY 624 ATGCCCAAGAGACGAGGCTGCGCAATGGCGTGAATGCGGATACCTGGGCGCAAGCGGCGCTG 683  
DB 601 ATGCCCAAGAGACGAGGCTGCGCAATGGCGTGAATGCGGATACCTGGGCGCAAGCGGCGCTG 660  
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DB 661 GCCCGGTCTTCTCATCGGATCAACAGACTGAGAGAGAGGGCGCTTGTGTACTCTGAC 720

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DB 1201 TAGTGCACTAGTTAAGTCAAAAAA 1230

RESULT 12  
US-09-989-721-356  
Sequence 356, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eacott, Dan L.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C55  
CURRENT APPLICATION NUMBER: US/09/989, 721  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
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DB 61 CTCAGAGTGGGGGAAATCTGAGCCCTGAGGCGCTTCTATCAGGCTGAGCTTCTGCA 120  
QY 144 CTGCTGCAATCTGAGCATCTCAGCCGCTGAGGAGAGCGCTGCTGTCAGATCTCTC 203  
DB 121 CTGCTGCAATCTGAGCATCTCAGCCGCTGAGGAGAGCGCTGCTGTCAGATCTCTC 180  
QY 204 GTTCCTGCTCTAAAGGGGATCGGGAGAGAAAGGAGGAGGAGGAGGAGGAGGAGG 263  
DB 181 GTTCCTGCTCTAAAGGGGATCGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
QY 264 GGAAGAGTGGGCGCCAGCGGAGAGAAAGGAGCATGGGGGAGCAAGAGGAGGAGT 323  
DB 241 GGAAGAGTGGGCGCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 300  
QY 324 GTGGTCTGTCATGAGAAATTTGGTCCATTGGCTCTAAAGTGAAGAGAGATTCGGT 383  
DB 301 GTGGTCTGTCATGAGAAATTTGGTCCATTGGCTCTAAAGTGAAGAGAGATTCGGT 360  
QY 384 GACATAGAGACCCCTGCTCTAATGAGAGAACAGGCTCTCCATGTGAGTGACGACGCTG 443  
DB 361 GACATAGAGACCCCTGCTCTAATGAGAGAACAGGCTCTCCATGTGAGTGACGACGCTG 420  
QY 444 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAGGTCACAGAGAGTCAAGTTC 503  
DB 421 CGCAAGGCGCATGGGGAGATGAGCAACAGGCTCTCAGGTCACAGAGAGTCAAGTTC 480  
QY 504 ATCAAGAAATGTGCTGCGCGGTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGAAATGTGCTGCGCGGTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAGAGAGAGCGTACGCGGAGCGCCAGCTGTCTGCAAGGCGCGGGGGGACGCTGAGC 623  
DB 541 GAGAGAGAGCGTACGCGGAGCGCCAGCTGTCTGCAAGGCGCGGGGGGACGCTGAGC 600  
QY 624 ATGCCCCAAGAGAGAGGCTGCAATGAGCTGAGAGCGGCTTACTGGCGGAGAGCGGCTG 683  
DB 601 ATGCCCCAAGAGAGAGGCTGCAATGAGCTGAGAGCGGCTTACTGGCGGAGAGCGGCTG 660  
QY 684 GCGCGTCTTCTATGCGGAGTCAACAGCTGAGAGAGAGAGGAGGAGGAGGAGGAGGAG 743  
DB 661 GCGCGTCTTCTATGCGGAGTCAACAGCTGAGAGAGAGAGGAGGAGGAGGAGGAGGAG 720

QY 744 CACTCCCGCATGCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTAGAC 803  
DB 721 CACTCCCGCATGCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTAGAC 780  
QY 804 GAGAGAGATCTGCTGAGAGATGGCTCGCGGCGGCTGGAACAGAGCTGCTGCAACC 863  
DB 781 GAGAGAGATCTGCTGAGAGATGGCTCGCGGCGGCTGGAACAGAGCTGCTGCAACC 840  
QY 864 ACCATGATCTTCAATGAGATTTGACAGAGAAACATGAGGCTCAGAGCTGGGGCTGC 923  
DB 841 ACCATGATCTTCAATGAGATTTGACAGAGAAACATGAGGCTCAGAGCTGGGGCTGC 900  
QY 924 CCATTGGGGGCGCCAGATGCTCTGAGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGCGCCAGATGCTCTGAGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCGAGGAGCTGCTGCTGTAAGGAGGAGGCTTCACTGAGTGAAGGCTGTGTCT 1043  
DB 961 CAGCGAGGAGCTGCTGCTGTAAGGAGGAGGCTTCACTGAGTGAAGGCTGTGTCT 1020  
QY 1044 AAATGAGAGAAATGGCTTATGCTTAAGAGAAATGAAGGCTTCTGGGGTGTGTCT 1103  
DB 1021 AAATGAGAGAAATGGCTTATGCTTAAGAGAAATGAAGGCTTCTGGGGTGTGTCT 1080  
QY 1104 TGAAGAGCAGAGTTTCACTGATATGAGCCCAATGCTCATTAATTAATTACC 1163  
DB 1081 TGAAGAGCAGAGTTTCACTGATATGAGCCCAATGCTCATTAATTAATTACC 1140  
QY 1164 CAGATGCTCTTCCATTAAGCTTGTGCTTGTCAAGCTATACATTAATTAATTACC 1223  
DB 1141 CAGATGCTCTTCCATTAAGCTTGTGCTTGTCAAGCTATACATTAATTAATTACC 1200  
QY 1224 TAGTCACTAGTTAAGTCAAAAAA 1253  
DB 1201 TAGTCACTAGTTAAGTCAAAAAA 1230

RESULT 13  
US-09-992-598-356  
Sequence 356, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Ealon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]



PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGAGAGCCCGCTTCGCTAGCGCGTCTCAGAGTGTGTCTCTGCTCGG 83  
 DB 1 GCGAGGCGAGAGCCCGCTTCGCTAGCGCGTCTCAGAGTGTGTCTCTGCTCGG 60  
 QY 84 CTCAGATGAGGGGGAATCTGAGCCCTGTGAGGCGTTCTAATCAGCCTGCTTCTGTC 143  
 DB 61 CTCAGATGAGGGGGAATCTGAGCCCTGTGAGGCGTTCTAATCAGCCTGCTTCTGTC 120  
 QY 144 CTGCTGCACTGAGCATCTCAGCGCGTGCAGTACAGCGCTGCTCTGTGAGATCTCTC 203  
 DB 121 CTGCTGCACTGAGCATCTCAGCGCGTGCAGTACAGCGCTGCTCTGTGAGATCTCTC 180  
 QY 204 GTCCCTGCTCAAAAGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
 DB 181 GTCCCTGCTCAAAAGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 QY 264 GGAAGAGTGGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
 DB 241 GGAAGAGTGGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 QY 324 GTGGGTGCTATGAGAAAATTGCTCCATTGCTCTAAAGTGAAGAAAGATTCGGT 383  
 DB 301 GTGGGTGCTATGAGAAAATTGCTCCATTGCTCTAAAGTGAAGAAAGATTCGGT 360  
 QY 384 GACATGAGAGCCCTGCTCTAATGAGAAACAGGCTCTCCATGTGAGTGCAGCCAGCTG 443  
 DB 361 GACATGAGAGCCCTGCTCTAATGAGAAACAGGCTCTCCATGTGAGTGCAGCCAGCTG 420  
 QY 444 GCGATGAGGCGGAGAGATGAGCAACAGGCTCTCAGCTACCAAGAGAGAGTCAAGTTC 503  
 DB 421 GCGATGAGGCGGAGAGATGAGCAACAGGCTCTCAGCTACCAAGAGAGAGTCAAGTTC 480  
 QY 504 ATCAAGATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGAGATCTACTGCTGTGAG 563  
 DB 481 ATCAAGATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGATCTACTGCTGTGAG 540  
 QY 564 GAGGAGAGAGCGCTAGCGGAGCGCCAGCTGTCTGTGCGAGGCGCGGCGGCGAGCTGAGC 623  
 DB 541 GAGGAGAGAGCGCTAGCGGAGCGCCAGCTGTCTGTGCGAGGCGCGGCGGCGAGCTGAGC 600  
 QY 624 ATGCCAAGAGAGAGCGCTGCAATGAGCGAGTGTGCGCGAGTCTGCGGCGAGCGGCGT 683  
 DB 601 ATGCCAAGAGAGAGCGCTGCAATGAGCGAGTGTGCGCGAGTCTGCGGCGAGCGGCGT 660  
 QY 684 GCCCGTGTCTTATCGGATCAACGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
 DB 661 GCCCGTGTCTTATCGGATCAACGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCATGCGGACCTTCAACAGTGGGCGAGCGGTGAGCCCAATATGCTTACGAC 803  
 DB 721 CACTCCCCCATGCGGACCTTCAACAGTGGGCGAGCGGTGAGCCCAATATGCTTACGAC 780  
 QY 804 GAGGAGAGCTCGTGGAGATGATGAGCTCGGCGGCTGGAACAGAGTGGCTTCCACACC 863  
 DB 781 GAGGAGAGCTCGTGGAGATGATGAGCTCGGCGGCTGGAACAGAGTGGCTTCCACACC 840  
 QY 864 ACCATGTACTTCATGTGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
 DB 841 ACCATGTACTTCATGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
 QY 924 CCATTGGGAGGCGCCCATGTCCTGTCAGAGGTTGGCAGGAGAGAGAGAGAGAGAGAGAG 983  
 DB 901 CCATTGGGAGGCGCCCATGTCCTGTCAGAGGTTGGCAGGAGAGAGAGAGAGAGAGAGAG 960  
 QY 984 CAGCCAGAGAGCTGTCTCTGTGAGAGGAGTGAAGGCTCAGTGAAGAGGCTGTGTCT 1043  
 DB 961 CAGCCAGAGAGCTGTCTCTGTGAGAGGAGTGAAGGCTCAGTGAAGAGGCTGTGTCT 1020  
 QY 1044 AAACCTGAGAAAATGCGCTATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103  
 DB 1021 AAACCTGAGAAAATGCGCTATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 QY 1104 TGAAGAGAGAGAGTTCATTAACCTGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1163  
 DB 1081 TGAAGAGAGAGAGTTCATTAACCTGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 QY 1164 CAGATTCCTCTTCATTAAG 1223  
 DB 1141 CAGATTCCTCTTCATTAAG 1200  
 QY 1224 TAGTCACTGATTAAGTCAAAAAA 1253  
 DB 1201 TAGTCACTGATTAAGTCAAAAAA 1230

RESULT 14  
 US-09-989-293A-356  
 Sequence 356, Application US/09989293A  
 Patent No. US20020177164A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Geider, Hanspeter  
 APPLICANT: Gerlt, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavini, Ivar J.  
 APPLICANT: Kijavini, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tamas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2730P1C66  
 CURRENT APPLICATION NUMBER: US/09/989,293A  
 CURRENT FILING DATE: 2001-11-20  
 PRIOR APPLICATION NUMBER: 60/049787

[illegible]

1 PRIOR FILING DATE: 1998-06-26  
2 PRIOR APPLICATION NUMBER: 60/090863  
3 PRIOR FILING DATE: 1998-06-26  
4 PRIOR APPLICATION NUMBER: 60/091360  
5 PRIOR FILING DATE: 1998-07-01  
6 PRIOR APPLICATION NUMBER: 60/091478  
7 PRIOR FILING DATE: 1998-07-02  
8 PRIOR APPLICATION NUMBER: 60/091544  
9 PRIOR FILING DATE: 1998-07-01  
10 PRIOR APPLICATION NUMBER: 60/091519  
11 PRIOR FILING DATE: 1998-07-02  
12 PRIOR APPLICATION NUMBER: 60/091626  
13 PRIOR FILING DATE: 1998-07-02  
14 PRIOR APPLICATION NUMBER: 60/091633  
15 PRIOR FILING DATE: 1998-07-02  
16 PRIOR APPLICATION NUMBER: 60/091978  
17 PRIOR FILING DATE: 1998-07-07  
18 PRIOR APPLICATION NUMBER: 60/091982  
19 PRIOR FILING DATE: 1998-07-07  
20 PRIOR APPLICATION NUMBER: 60/092182  
21 PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY	24	GCAGCGGGCAGGACCCCGCTTGCTGACCTACCGGTCTCAGAGATTGATGCTCGCTGCG	83
Db	1	GGGAGGGGCGAGGACCCCGCTTGCTGACCGGTCTCAGAGATTGATGCTCGCTGCG	60
OY	84	CTCAGGATGAGGGGGGAAATTGGACCTTGTTGGGCGTTCTAATCAGCCTTGACTTCTGTCA	143
Db	61	CTCAGGATGAGGGGGGAAATTGGACCTTGTTGGGCGTTCTAATCAGCCTTGACTTCTGTCA	120
OY	144	CTGCTGGCATCTGGAATCTCAGCCGGTGGGAGATGAGCGCGCTCTGTGCGAGATCTTC	203
Db	121	CTGCTGGCATCTGGAATCTCAGCCGGTGGGAGATGAGCGCTCTGTGTGCGAGATCTTC	180
OY	204	GTCCTTGGCTTCAAGGGGATGCGGAGAGAAAGGAGACAAAGCGCCCTCCGACGGCCT	263
Db	181	GTCCTTGGCTTCAAGGGGATGCGGAGAGAAAGGAGACAAAGCGCCCTCCGACGGCCT	240
OY	264	GGAAAGTCTGGGCCCCACGGGAGAAAAGAGACATGGGGGACAAAGACAGAAAGGCACGT	323
Db	241	GGAAAGTCTGGGCCCCACGGGAGAAAAGAGACATGGGGGACAAAGACAGAAAGGCACGT	300
OY	324	GTCGGTCTGTCATGGAATAATTGATCCCATTTGCTCTAAGGTGAGAAAGAGATTCCGCT	383
Db	301	GTCGGTCTGTCATGGAATAATTGATCCCATTTGCTCTAAGGTGAGAAAGAGATTCCGCT	360
OY	384	GACATAGGACCCCCCTGGTCTTAATGGAGAACCAAGGCTTCCATGTGATGATGACCCACGCTG	443
Db	361	GACATAGGACCCCCCTGGTCTTAATGGAGAACCAAGGCTTCCATGTGATGATGACCCACGCTG	420
OY	444	CGCAAGGCCATGCGGGGAGATGGACAAACGAGTCTCAGCTGACGAGCGACGTCAAGTTTC	503
Db	421	CGCAAGGCCATGCGGGGAGATGGACAAACGAGTCTCAGCTGACGAGCGACGTCAAGTTTC	480
OY	504	ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGGAGAGCAAGATCTAACCCTGTGTGAAG	563
Db	481	ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGGAGAGCAAGATCTAACCCTGTGTGAAG	540
OY	564	GAGGAGAAAGCGTTACGGCGGACGCCCAAGCTGTCTGCGAAGGCCGCGGGGGCAAGCTGAGC	623
Db	541	GAGGAGAAAGCGTTACGGCGGACGCCCAAGCTGTCTGCGAAGGCCGCGGGGGCAAGCTGAGC	600
OY	624	ATGCCCAAGAGCAGAGCTTCCAAATGGCTTGATGGCCGATACCTTGGCGCACGCCGCTTG	683
Db	601	ATGCCCAAGAGCAGAGCTTCCAAATGGCTTGATGGCCGATACCTTGGCGCACGCCGCTTG	660
OY	684	GCCCTGTCTTCAATGGGATCAACGACTCTGAGAGAAAGAGGGCGCTTTCGTGTACTTGAC	743
Db	661	GCCCTGTCTTCAATGGGATCAACGACTCTGAGAGAAAGAGGGCGCTTTCGTGTACTTGAC	720

QY	744	CACCTCCCCCAATGCGGAGACCTTTCAACAAGGCGCGACGCGGTGAGGCCCAACAATGCGCTACGAC	803
Db	721	CACCTCCCCCAATGCGGAGACCTTTCAACAAGGCGCGACGCGGTGAGGCCCAACAATGCGCTACGAC	780
QY	804	GAGGAGGAGCTGCGGTGAGATGAGTGGGCTTCGGGCGGCTGGAAACGACGTGGCTGCGCACACC	863
Db	781	GAGGAGGAGCTGCGGTGAGATGAGTGGGCTTCGGGCGGCTGGAAACGACGTGGCTGCGCACACC	840
QY	864	ACCATGTAATCTTCATGTGTGAGTTTGACAGAGGAAACATGTGAGCTTCAGGCTGGGGGCTGC	923
Db	841	ACCATGTAATCTTCATGTGTGAGTTTGACAGAGGAAACATGTGAGCTTCAGGCTGGGGGCTGC	900
QY	924	CCATTGGGGGGGCCCCACATGTCCTTGCAAGGGTTGGCAGGGAGCAGAGGCCACGATGGTGC	983
Db	901	CCATTGGGGGGGCCCCACATGTCCTTGCAAGGGTTGGCAGGGAGCAGAGGCCACGATGGTGC	960
QY	984	CAGCCAGGGAGCTGTCCCTCTGTGAAAGGGTGGAGGCTCCTGAGTGAAGGGCTGTGTCT	1043
Db	961	CAGCCAGGGAGCTGTCCCTCTGTGAAAGGGTGGAGGCTCCTGAGTGAAGGGCTGTGTCT	1020
QY	1044	AAACTGAGAAAATGGCCTTAATGCTTAAAGAGGAAAATGAAAAGTTCCTGGGGTGTCTGTCTC	1103
Db	1021	AAACTGAGAAAATGGCCTTAATGCTTAAAGAGGAAAATGAAAAGTTCCTGGGGTGTCTGTCTC	1080
QY	1104	TGAAGAAACAGAGTTTCACTACCTGTATGTAGGCCCAATGCTCAATTAATTAATTATACC	1163
Db	1081	TGAAGAAACAGAGTTTCACTACCTGTATGTAGGCCCAATGCTCAATTAATTAATTATACC	1140
QY	1164	CAGAAATGCTCTTCATTAAGCTTGTGCTTGTGTCAGAGCTATACAATTAATCTTTAAG	1223
Db	1141	CAGAAATGCTCTTCATTAAGCTTGTGCTTGTGTCAGAGCTATACAATTAATCTTTAAG	1200
QY	1224	TAGTGCAGTACTTAAGTCCAAAAA	1253
Db	1201	TAGTGCAGTACTTAAGTCCAAAAA	1230

1	PRIOR APPLICATION NUMBER: 60/089440
2	PRIOR FILING DATE: 1998-06-16
3	PRIOR APPLICATION NUMBER: 60/089512
4	PRIOR FILING DATE: 1998-06-15
5	PRIOR APPLICATION NUMBER: 60/089514
6	PRIOR FILING DATE: 1998-06-16
7	PRIOR APPLICATION NUMBER: 60/089532
8	PRIOR FILING DATE: 1998-06-17
9	PRIOR APPLICATION NUMBER: 60/089538
10	PRIOR FILING DATE: 1998-06-17
11	PRIOR APPLICATION NUMBER: 60/089598
12	PRIOR FILING DATE: 1998-06-17
13	PRIOR APPLICATION NUMBER: 60/089599
14	PRIOR FILING DATE: 1998-06-17
15	PRIOR APPLICATION NUMBER: 60/089600
16	PRIOR FILING DATE: 1998-06-17
17	PRIOR APPLICATION NUMBER: 60/089653
18	PRIOR FILING DATE: 1998-06-17
19	PRIOR APPLICATION NUMBER: 60/089801
20	PRIOR FILING DATE: 1998-06-18
21	PRIOR APPLICATION NUMBER: 60/089907
22	PRIOR FILING DATE: 1998-06-18
23	PRIOR APPLICATION NUMBER: 60/089908
24	PRIOR FILING DATE: 1998-06-18
25	PRIOR APPLICATION NUMBER: 60/089947
26	PRIOR FILING DATE: 1998-06-19
27	PRIOR APPLICATION NUMBER: 60/089948
28	PRIOR FILING DATE: 1998-06-19
29	PRIOR APPLICATION NUMBER: 60/089952
30	PRIOR FILING DATE: 1998-06-19
31	PRIOR APPLICATION NUMBER: 60/090246
32	PRIOR FILING DATE: 1998-06-22
33	PRIOR APPLICATION NUMBER: 60/090252
34	PRIOR FILING DATE: 1998-06-22
35	PRIOR APPLICATION NUMBER: 60/090254
36	PRIOR FILING DATE: 1998-06-22
37	PRIOR APPLICATION NUMBER: 60/090349
38	PRIOR FILING DATE: 1998-06-23
39	PRIOR APPLICATION NUMBER: 60/090355
40	PRIOR FILING DATE: 1998-06-23
41	PRIOR APPLICATION NUMBER: 60/090429
42	PRIOR FILING DATE: 1998-06-24
43	PRIOR APPLICATION NUMBER: 60/090431
44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/090435
46	PRIOR FILING DATE: 1998-06-24
47	PRIOR APPLICATION NUMBER: 60/090444
48	PRIOR FILING DATE: 1998-06-24
49	PRIOR APPLICATION NUMBER: 60/090445
50	PRIOR FILING DATE: 1998-06-24
51	PRIOR APPLICATION NUMBER: 60/090472
52	PRIOR FILING DATE: 1998-06-24
53	PRIOR APPLICATION NUMBER: 60/090535
54	PRIOR FILING DATE: 1998-06-24
55	PRIOR APPLICATION NUMBER: 60/090540
56	PRIOR FILING DATE: 1998-06-24
57	PRIOR APPLICATION NUMBER: 60/090542
58	PRIOR FILING DATE: 1998-06-24
59	PRIOR APPLICATION NUMBER: 60/090557
60	PRIOR FILING DATE: 1998-06-24
61	PRIOR APPLICATION NUMBER: 60/090676
62	PRIOR FILING DATE: 1998-06-25
63	PRIOR APPLICATION NUMBER: 60/090678
64	PRIOR FILING DATE: 1998-06-25
65	PRIOR APPLICATION NUMBER: 60/090690
66	PRIOR FILING DATE: 1998-06-25
67	PRIOR APPLICATION NUMBER: 60/090694
68	PRIOR FILING DATE: 1998-06-25
69	PRIOR APPLICATION NUMBER: 60/090695
70	PRIOR FILING DATE: 1998-06-25
71	PRIOR APPLICATION NUMBER: 60/090696
72	PRIOR FILING DATE: 1998-06-25
73	PRIOR APPLICATION NUMBER: 60/090682



**This Page Blank (uspto)**









Db 247 AGGTCAACAGAGCCCGGCGCTTCTGAGAGAGAGAC 287

RESULT 7  
US-09-215-681-273  
Sequence 273, Application US/09215681A  
Patent No. 6528253  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Frudakis, Tony N.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
FILE REFERENCE: 210121.463  
CURRENT FILING DATE: 1998-12-17  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 273  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(579)  
OTHER INFORMATION: n = A,T,C or G  
US-09-215-681-273

Query Match 5.3%; Score 66.8; DB 4; Length 579;  
Best Local Similarity 52.0%; Pred. No. 2.4e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Qy 140 GTCACCTGCTGCATCTGAGACATCTCCAGCCGCTGGCGCATGACCCCTGCTGTGCAGAT 199  
Db 7 GTCCGGGCGGAGTGTGCGCTCTCTGCGAAGCTGGTGAATGATGATCACTCTGAAAAACC 66  
Qy 200 CCTGCTCCCTGCGCTCAAGGGAGATCGGAGAGAGAGAGACAAAGCGCCCGCGAGC 259  
Db 67 CGAGACACTGCTGTAGAGAGAGATTTGTGACACAGAGTCTCTGTTTCCCTGGAAC 126  
Qy 260 GCTTGAAGAGTGGGCCCCCAGGAGAGAAAAAGAGACATGGGGGACAAAGACAGAAAG 319  
Db 127 TCCCTGAGCTTCTGCTTCAAGGATTAAGGAGACACATGCTGTGATGATGAAAGG 186  
Qy 320 CAGTGTGGGCTGATGAGAAAAATTTGTCATGAGCTTAAAGTGAAGAGAGATTC 379  
Db 187 ACAGCCCGGTCTCTGCTGTGAGAGGTGAACCTGAGGCCCTGTGTGAATGGAATCC 246  
Qy 380 CGGTGACATAGACCCCTGTGTCTTAATGAGAACAGGCC 420  
Db 247 AGGTCAACAGAGCCCGGCGCTTCTGAGAGAGAGAC 287

RESULT 8  
US-09-216-003A-273  
Sequence 273, Application US/09216003A  
Patent No. 6670463  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Frudakis, Tony N.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER  
FILE REFERENCE: 210121.462  
CURRENT FILING DATE: 1998-12-17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 273  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: modified\_base

LOCATION: (223)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (265)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (277)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (308)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (329)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (346)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (360)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (366)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (429)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (448)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (517)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (524)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (531)  
OTHER INFORMATION: Where n is a, c, g or t  
NAME/KEY: modified\_base  
LOCATION: (578)  
OTHER INFORMATION: Where n is a, c, g or t  
US-09-216-003A-273

Query Match 5.3%; Score 66.8; DB 4; Length 579;  
Best Local Similarity 52.0%; Pred. No. 2.4e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Qy 140 GTCACCTGCTGCATCTGAGACATCTCCAGCCGCTGGCGCATGACCCCTGCTGTGCAGAT 199  
Db 7 GTCCGGGCGGAGTGTGCGCTCTCTGCGAAGCTGGTGAATGATGATCACTCTGAAAAACC 66  
Qy 200 CCTGCTCCCTGCGCTCAAGGGAGATCGGAGAGAGAGAGACAAAGCGCCCGCGAGC 259  
Db 67 CGAGACACTGCTGTAGAGAGAGATTTGTGACACAGAGTCTCTGTTTCCCTGGAAC 126  
Qy 260 GCTTGAAGAGTGGGCCCCCAGGAGAGAAAAAGAGACATGGGGGACAAAGACAGAAAG 319  
Db 127 TCCCTGAGCTTCTGCTTCAAGGATTAAGGAGACACATGCTGTGATGATGAAAGG 186  
Qy 320 CAGTGTGGGCTGATGAGAAAAATTTGTCATGAGCTTAAAGTGAAGAGAGATTC 379  
Db 187 ACAGCCCGGTCTCTGCTGTGAGAGGTGAACCTGAGGCCCTGTGTGAATGGAATCC 246  
Qy 380 CGGTGACATAGACCCCTGTGTCTTAATGAGAACAGGCC 420  
Db 247 AGGTCAACAGAGCCCGGCGCTTCTGAGAGAGAGAC 287

RESULT 9  
US-09-667-857-273  
Sequence 273, Application US/09667857  
Patent No. 669664  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
APPLICANT: Vedick, Thomas S.  
APPLICANT: Carter, Derrick  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C5  
CURRENT APPLICATION NUMBER: US/09/667,857  
CURRENT FILING DATE: 2000-09-20  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 273  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(579)  
OTHER INFORMATION: n = A,T,C or G  
US-09-667-857-273

Query Match 5.3%; Score 66.8; DB 4; Length 579;  
Best Local Similarity 52.0%; Pred. No. 2.4e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 140 GTCACTGTCGCCATCTGAGATCCCTCAGCCGCTGGCCATGAGCGCTGTCGTGACAT 199  
DB 7 GTCCGCGCCGAGGCTGTGCTGCTCTGCGGAGGCTGTGAGTGTACCCCTGGAACC 66  
QY 200 CCTCTCCCTGCTCTCAAGGGATGCGGAGAGAGGAGCAAGGCGCCCGGAGC 259  
DB 67 CGGAGAGCTGTGAGAGAGAGTGTGACACAGGGTGTCTGTGTTCCCTGGAAC 126  
QY 260 GCCTGGAAGTTCGCGCCCAAGGAGAGAGAGATGAGGAGCAAGGAGAGAG 319  
DB 127 TCTGTGACTTCTGCTTCAAGGATGAGGAGACATGTGTGATGATGAGG 186  
QY 320 CAGTGTGGTGTCTGAGAGAAATGTCCTTGGCTTAAGGTGAGAGAGATTC 379  
DB 187 ACAGCCCGGTCTCTGTGTGAGAGGTGAACCTGAGCCCTGTGAAATGGAATCC 246  
QY 380 CGGTGACATAGAGCCCTGTGTCTTAATGAGAGACAGGCC 420  
DB 247 AGGTCAACAGAGGCCCGGCTTCTGTGAGAGAGAGAC 287

RESULT 10  
US-08-392-367B-1  
Sequence 1, Application US/08392367B  
Patent No. 5691197  
GENERAL INFORMATION:  
APPLICANT: Trygvaeson, Karl  
APPLICANT: Elomaa, Outi  
APPLICANT: Kangas, Maarit  
TITLE OF INVENTION: An Inolated DNA Sequence For a  
Patent No. 5691197  
TITLE OF INVENTION: No. 5691197 Macrophage Receptor with  
TITLE OF INVENTION: a Collagenous Domain and the  
TITLE OF INVENTION: Polypeptide Chain Encoded by  
TITLE OF INVENTION: such a Sequence  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
CITY: Cleveland  
STATE: Ohio

COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch,  
MEDIUM TYPE: 720 Kb securable  
COMPUTER: IBM PS/2, Model 35 SX  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,367B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: TRV 2 009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
TELEX: (216) 980162  
INFORMATION FOR SEQ ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1868 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Nucleotide-genomic DNA  
HYPOTHEICAL: No. 5691197 relevant  
ANTI-SENSE: No. 5691197 relevant  
US-08-392-367B-1

Query Match 5.3%; Score 65.8; DB 1; Length 1868;  
Best Local Similarity 52.3%; Pred. No. 8e-08;  
Matches 145; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 151 CATCTGACATCTCTCAGCCGCTGCGATGAGCGCTGCTGTGACATCTCTGCTCCTG 210  
DB 809 CACTGTGTCTCAGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868  
QY 211 GCTCTAAAGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270  
DB 869 GCCCAAGGGGAG 928  
QY 271 TCGGCCCCAGGAG 330  
DB 929 AAGGAGATGAG 988  
QY 331 GTCATGAGAAATGTCCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390  
DB 989 GTAAAGGTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048  
QY 391 GACCCCTGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427  
DB 1049 GTAGCAAGAGAAACCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1085

RESULT 11  
US-08-893-467A-1  
Sequence 1, Application US/08893467A  
Patent No. 6063901  
GENERAL INFORMATION:  
APPLICANT: Trygvaeson, Karl  
APPLICANT: Elomaa, Outi  
APPLICANT: Kangas, Maarit  
TITLE OF INVENTION: An Inolated DNA Sequence For a  
Patent No. 6063901  
TITLE OF INVENTION: No. 6063901 Macrophage Receptor with  
TITLE OF INVENTION: a Collagenous Domain and the  
TITLE OF INVENTION: Polypeptide Chain Encoded by  
TITLE OF INVENTION: such a Sequence  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,

ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
STREET: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch,  
COMPUTER: IBM PS/2, Model 35 SX  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893.467A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/ROCKET NUMBER: TRV 2 009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1868 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Nucleotide-genomic DNA  
HYPOTHETICAL: No. 6063901 relevant  
ANTI-SENSE: No. 6063901 relevant  
US-08-893-467A-1

Query Match 5.3%; Score 65.8; DB 3; Length 1868;  
Best Local Similarity 52.3%; Pred. No. 8e-08;  
Matches 145; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 151 CATCTGACATCTTCAGCGCGCTGCGATGACGCTGCTGTGCAATCCTCGTCCCTG 210  
DB 809 CAACTGTGCTCCAGCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868  
QY 211 GCCTCAAGGGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270  
DB 869 GCCCAAGGGGAG 928  
QY 271 TCGGCCCCAGGAG 330  
DB 929 AAGGGGAG 988  
QY 331 GTCAATGAG 390  
DB 989 GTAAAGGAG 1048  
QY 391 GACCCCTGTGCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427  
DB 1049 GTGACCAAG 1085

RESULT 12  
US-09-404-879A-274/c  
Sequence 274, Application US/09404879A  
Patent No. 6468546  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C2  
CURRENT APPLICATION NUMBER: US/09/404.879A

CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 393  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 274  
LENGTH: 330  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(330)  
OTHER INFORMATION: n = A,T,C or G  
US-09-404-879A-274

Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 140 GTCACTGCTCCATCTGACATCTCAGCCGCTGCGATGACGCTGCTGTGACAGAT 199  
DB 324 GTGCGGCGAG 265  
QY 200 CTTGCTCTGCGCTCAAAGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAG 259  
DB 264 CGAGCACTGTGAG 205  
QY 260 GCGTGAAGAGTGGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319  
DB 204 TCTTGACCTTCTGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 145  
QY 320 CAGTGTGGTCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 379  
DB 144 ACAGCCGGGTCTCTGTGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 85  
QY 380 CGGTGACATGAG 420  
DB 84 AGGTCAACAG 44

RESULT 13  
US-09-338-933-274/c  
Sequence 274, Application US/09338933  
Patent No. 6488931  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer Lynn  
APPLICANT: King, Gordon E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF  
FILE REFERENCE: 210121.462C1  
CURRENT APPLICATION NUMBER: US/09/338.933  
NUMBER OF SEQ ID NOS: 312  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 274  
LENGTH: 330  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(330)  
OTHER INFORMATION: n = A,T,C or G  
US-09-338-933-274

Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 140 GTCACTGCTCCATCTGACATCTCAGCCGCTGCGATGACGCTGCTGTGACAGAT 199  
DB 324 GTGCGGCGAG 265  
QY 200 CTTGCTCTGCGCTCAAAGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAG 259  
DB 264 CGAGCACTGTGAG 205

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us-09-806-277a-13.rn1

Page 7

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QY 260 GCTTGAGAGAGTCGGCCCCAAGGAGAGAAAGAGACATGGGGGACAAAGAGCAGAAAG 319
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Db 204 TCTGGAGCTTCTGGCTTCAAGGATTAAGGAGACATGCTGAGATGATTAAGAGG 145
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QY 320 CAGTGTGGTGTCTATGAGAAATTTGTCCTTGGCTCTAAAGGTGAGAAAGAGATTTC 379
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Db 144 ACAAGCCGGTGTCTCTGGTGTGAAGGTGAACCTGTGCCCCCTGTGTAATGGAATCC 85
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QY 380 CGGTGACATAGAACCCCTGTCTTAATGAGAACCAAGGCC 420
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Db 84 AGTCAAAACAGAGCCCGTGGCTTCTGTGTGAGAGAGAC 44
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RESULT 14  
US-09-215-681-274/C  
; Sequence 274, Application US/09215681A  
; Patent No. 6528253  
; GENERAL INFORMATION:  
; APPLICANT: MITCHEM, Jennifer L.  
; APPLICANT: FRUDEKIS, Tony N.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
; FILE REFERENCE: 210121.463  
; CURRENT APPLICATION NUMBER: US/09/215,681A  
; NUMBER OF FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 310  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 274  
; LENGTH: 330  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(330)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-215-681-274

Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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QY 140 GTCACTGTGTCATCTGACATCTCCACGCGCTGGCATGACGCTGTCTGTGCAAT 199
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Db 264 CGGACGACCTGTGTGAAGAGAGATTGTGACCAAGGTGCTGTGTTTCCCTGGAAC 205
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QY 260 GCTTGAAGAGTCGGCCCCAAGGAGAGAAAGAGACATGGGGGACAAAGACAGAAAG 319
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Db 204 TCTTGACTTCTCTGGCTTCAAGGATTAAGGAGCAATGATGATGATGAAGGG 145
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RESULT 15  
US-09-216-003A-274/C  
; Sequence 274, Application US/09216003A  
; Patent No. 6670463  
; GENERAL INFORMATION:  
; APPLICANT: MITCHEM, Jennifer L.  
; APPLICANT: FRUDEKIS, Tony N.  
; APPLICANT: KING, Gordon B.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER

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; FILE REFERENCE: 210121.462  
; CURRENT APPLICATION NUMBER: US/09/216,003A  
; CURRENT FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 310  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 274  
; LENGTH: 330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified_base  
; LOCATION: (171)  
; OTHER INFORMATION: where n is a, c, g or t  
US-09-216-003A-274
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Query Match 5.2%; Score 65.6; DB 4; Length 330;  
Best Local Similarity 52.0%; Pred. No. 3.8e-08;  
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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Db 324 GTGGGCGCGAGGTGTGGCTCTCTGGCAAGGCTGTGAAGTGTCACTCGAATAACC 265
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QY 200 CCTGCTCCCTGGCTCAAAAGGGATGCGGAGAGAAAGGACAAAGCGCCCCGAGC 259
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Db 264 CGGACGACCTGTGTGAAGAGAGATTGTGACCAAGGTGCTGTGTTTCCCTGGAAC 205
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QY 260 GCTTGAAGAGTCGGCCCCAAGGAGAGAAAGAGACATGGGGGACAAAGACAGAAAG 319
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Db 204 TCTTGACTTCTCTGGCTTCAAGGATTAAGGAGCAATGATGATGATGAAGGG 145
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Db 144 ACAAGCCGGTGTCTCTGGTGTGAAGGTGAACCTGTGCCCCCTGTGTAATGGAATCC 85
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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41	271	100.0	1238	10	US-09-987-559-356	Sequence 356, App
42	271	100.0	1238	10	US-09-997-601-356	Sequence 356, App
43	271	100.0	1238	10	US-09-990-443-356	Sequence 356, App
44	271	100.0	1238	10	US-09-991-654-356	Sequence 356, App
45	271	100.0	1238	10	US-09-997-628-356	Sequence 356, App

## ALIGNMENTS

RESULT 1  
US-10-258-105-45  
Sequence 45, Application US/10258105  
Publication No. US20030158382A1  
GENERAL INFORMATION:  
APPLICANT: Wakamiya et al.  
TITLE OF INVENTION: No. US20030158382A1 Collectin  
FILE REFERENCE: 19036/38785  
CURRENT APPLICATION NUMBER: US/10/258,105  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: PCT/JP01/03468  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: JP 2000-120358  
PRIOR FILING DATE: 2000-04-21  
NUMBER OF SEQ ID NOS: 61  
SEQ ID NO 45  
LENGTH: 813  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-10-258-105-45

## Alignment Scores:

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Score:	271.00	Matches:	271
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-806-277a-6 (1-271) x US-10-258-105-45 (1-813)

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Db 1 ATGAGGGGGAATCTGGCCCTGCTGGCTTATCTACGCTGGCTTCTCTCTCTGCTG 60
QY 21 ProSerGlyHisProGlnProAlaGlyAspMetGlyAspSerValGlnIleLeuValPro 40
Db 21 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACCGCTGCTGCTGAGATCTCTGCTCCT 120
QY 41 GlyLeuMetGlyAspAlaGlyGlyValGlyAspGlyValAspProGlyArgProGlyArg 60
Db 41 GGCTCAAGGGGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 61 ValGlyProThrGlyGlyValGlyValAspMetGlyAspGlyGlyGlyValGlySerValGly 80
Db 61 GTGGGCCCCACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100
Db 81 CGTATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProGlyGlyGlyGlyGlyGlyGlyGly 120
Db 101 GGAGCCCTCTGCTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlnLeuValPheIleLys 140
Db 121 GCCATCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 141 AsnAlaValAlaGlyValArgGlyThrGlySerValGlyValGlyValGlyValGlyVal 160
Db 141 AATCTGTCGGCGGTGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 161 LysArgTyrValAspAlaGlnLeuSerCysGlnGlyArgGlyGlyTyrThrLeuSerMetPro 180
Db 161 AAGGCGCTACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 181 LysAspGlyAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyValLeuAlaArg 200
Db 181 AAGGACGAGGCTGCCAATGGCTGATGGCCGATACCTGGCGAGAGAGAGAGAGAGAG 600
QY 201 ValIleIleGlyIleAsnAspLeuGlnGlyValAlaPheValTyrSerAspHisSer 220
Db 201 GTCTTCATCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 221 ProMetArgTyrPheAsnLysTyrPheSerGlyGlyProAsnAlaAlaTyrAspGlyGly 240
Db 221 CCCTACGCGAGACTTCAACAGTGGGCGAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 241 AspCysValGlyMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThMet 260
Db 241 GACTGCGTGGAGATGTGGCTCGGCGCGGTGGAACGAGCTGGCTGCACACACATG 780
QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271
Db 261 TACTTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813
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## RESULT 2

US-09-989-722-356  
Sequence 356 Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989, 722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 2,98e-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-722-356 (1-1238)

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Db 127 CCAATCTGACATCTCTACGCCGCTGGCGATACCCCTCTCTGTGCAATCTCTGCTCCT 186  
QY 41 GlyLeuLysGlyAspAlaGlyGlnLysGlyAspLysGlyAlaProGlyArgProGlyArg 60  
Db 187 GGCCTCAAGGGGATGCGGAG 246  
QY 61 ValGlyProThrGlyGlnLysGlyAspMetCylAspLysGlyGlnLysGlySerValGly 80



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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Score: 2,988-269 Length: 1238  
Percent Similarity: 271.00 Matches: 271  
Best Local Similarity: 100.00% Conservative: 0  
Query Match: 100.00% Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-723-356 (1-1238)

QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuLLeSerLeuAlaPheLeuSerLeu 20  
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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCACTGTGACATCTCTACCGCGCTGGCATACCGCTCTGTGCAGATCTGTCCCT 186  
QY 41 GlyLeuYsgIYAspAlaGlyGlyLeuYsgIYAspYsgIYAlaProGlyYArgProGlyYArg 60  
DB 187 GGCCTCAAGGGGATGCGGAG 246  
QY 61 ValGlyProThrGlyGlyLeuYsgIYAspMetGlyAspYsgIYGlyIleYsgIYSerValGly 80  
DB 247 GTCCGCCCAAGGAG 306  
QY 81 ArgHisGlyYsIleGlyProIleGlySerYsgIYGlyYsgIYAspSerGlyYAspIle 100  
DB 307 CGTCAATGAGAAATTTGCTCCATTGGCTCTAAAGTGAAGAAAGAGATTCCGGTGACAT 366  
QY 101 GlyProProGlyProAsnGlyGlyLeuProGlyLeuProCysGlyCysSerGlyLeuArgIys 120  
DB 367 GACCCCTGTGCTTAATGAG 426  
QY 121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlyLeuLeuPheIleYs 140  
DB 427 GCCATCGGGAG 486  
QY 141 AsnAlaValAlaGlyValArgGlyThrGlySerYsIleYrLeuLeuValYsGlyGly 160  
DB 487 AATGCTGTCCCGGTGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LysArgYrYrAlaAspAlaGlnLeuSerCysGlnGlyYrYrGlyYrYrLeuSerMetPro 180  
DB 547 AAGCGCTACGGGAG 606

QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGACACAGGCTGCGCAATGGCTGATGGCCCAATACCTGGCGCAAGCGGCTGGCCCGT 666  
QY 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCATCGGCATCAACGACCTGAGAGAGAGGCGGCTTCGTGTACTGTGACCACTCC 726  
QY 221 ProMetArgThrPheAsnLysTyrArgSerGlyLysProAsnAsnAlaTyrAspGluGlu 240  
Db 727 CCCATCGGACCTTCAACAAGTGGCGAGCGGTGAGCCCAACATGCTACGACGAGAG 786  
QY 241 AspCysValGluMetValAlaSerGlyGlyTyrPheAsnValAlaCysHisThrMet 260  
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QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 847 TACTTCATGTGTGAGTTTGACAGAGAACATG 879  
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US-09-989-279-356  
Sequence 356, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C56  
CURRENT APPLICATION NUMBER: US/09/989, 279  
CURRENT FILING DATE: 2001-11-19  
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 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deenoyers, Luc  
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 APPLICANT: Watanabe, Collin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
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; PRIOR FILING DATE: 1998-07-09

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QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
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PRIOR FILING DATE: 1998-06-25



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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 2,986-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-731-356 (1-1238)

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67 ATGAGGGGGAATCTGGCCCTGGTGGCGTTCTTAACAGCCCTTCTTCTGACATGCTG 126  
21 ProSerGlyHLeuProGlyProAlaGlyAspAlaCySerValGlnIleLeuValPro 40  
127 CCATCTGACATCTCTCAAGCCGGCTGGCGATGACGCTGCTGTGACATCTCTCCCT 186  
41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 60  
187 GGCCTCAAGAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
61 ValGlyProThGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
247 GTCCGCCCCCAAGGAG 306  
81 ArgHLeuValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
307 COTCATGAGAAATATGCTCCATGCTCTTAAGGTGAGAGAGAGAGAGAGAGAGAGAG 366  
101 GlyProProGlyProAsnGlyValGlyValGlyValGlyValGlyValGlyValGly 120  
367 GAGCCCTCTGTGCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
121 AlaIleGlyValMetAspAsnGlnValSerGlnLeuThrSerGlnLeuValPheIle 140  
427 GCCATCGGGGAGATGACACCAAGATCTCTCAAGCTGACCGAGAGAGAGAGAGAGAG 486  
141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyVal 160  
487 AATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546

161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValGlyValGlyValGlyValGly 180  
547 AAGGCTACGCGAGCGCCAGCTGCTCCAGAGGCGCGGAGAGAGAGAGAGAGAGAGAG 606  
181 LysAspGluAlaAlaAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 200  
607 AAGGAG 666  
201 ValPheIleGlyValLeuAsnLeuGlyValGlyValGlyValGlyValGlyValGlyVal 220  
667 GCTTCATCGGACCAACAG 726  
221 ProMetArgThrPheAsnLeuValGlyValGlyValGlyValGlyValGlyValGlyVal 240  
727 CCATGCGGACCTTCAACAG 786  
241 AspCysValGluMetValAlaSerGlyValGlyValGlyValGlyValGlyValGlyVal 260  
787 GACTGCGGAG 846  
261 TyrPheMetCysGluPheAspGlyGluAsnMet 271  
847 TACTTCATGTGTGAGTTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

RESULT 7  
US-09-989-732-356  
Sequence 356, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
CURRENT APPLICATION NUMBER: US/09/989, 732  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322

[illegible]

1 PRIOR FILING DATE: 1998-07-02  
 2 PRIOR APPLICATION NUMBER: 60/091978  
 3 PRIOR FILING DATE: 1998-07-07  
 4 PRIOR APPLICATION NUMBER: 60/091982  
 5 PRIOR FILING DATE: 1998-07-07  
 6 PRIOR APPLICATION NUMBER: 60/092182  
 7 PRIOR FILING DATE: 1998-07-09

### Alignment Scores:

Pred. No.:	2,986-269	Length:	1230
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Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
GB:	9	Gaps:	0

US-09-806-277A-6 (1-271) x US-09-989-732-356 (1-1238)

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QY	21	ProSeRG1yH1aProG1nPro1aG1yAaAPaPa1aCySeSerValG1n1eLeuValPro	40
Db	127	CCATCTGGACATCTCTCAAGCGGCTGGCGCATGACGCTGCTCTGTGTGCAATCTGTGCTT	186
QY	41	G1yLeu1ySeG1yAaPa1aG1yG1u1ySeG1yAaP1ySeG1yVal1aProG1yAaPProG1yAaG	60
Db	187	GGCGCTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGCGCGCCCGGACGGCGCTGGAAAG	246
QY	61	ValG1yProthRG1yG1u1ySeG1yAaPMeTG1yAaP1ySeG1yG1n1ySeValG1y	80
Db	247	GTCGGCCCCACGGGAGAAAGAGACATGGGGGACAAAGAGCAAGAGAGGCAAGTGTGGGT	306
QY	81	ArgH1SeG1yLys1leG1yPro1leG1ySe1ySe1yG1yG1u1ySeG1yAaSPSeG1yAaP1le	100
Db	307	CGTCATGGAAAATTTGGTCCCATGTGCTCTTAAGGAGAAAGAGAAAGATTCCGGTGACATA	366
QY	101	G1yProProG1yProAaenG1yG1uPProG1yLeuProCySeG1uCySeSerG1nLeuA1yLys	120
Db	367	GGAGCCCCCTGGTCTTAATGAGAGAACAGCGCTCCCATGTGATGACGACCACTCGCAG	426
QY	121	Ala1leG1yG1uMeArPaPaenG1nVal1SeRG1nLeuThSeRG1nLeu1yPhe1leLys	140
Db	427	GCCATCGGGAGATGAGCAACAGGCTCTTCAAGCTGACCAAGAGACTTAAGTTATCAAG	486
QY	141	AaPa1aVal1aG1yVal1aRG1uThRG1uSe1y1e1yLeuLeuVal1yG1uG1u	160
Db	487	AATGCTGTGTGGCGGTGGCGGAGACGAGAGCAAGATCTACCTGCTGTAAAGAGAG	546
QY	161	LysAaRG1yA1aAaPa1aG1nLeuSeRCySeG1nG1yAaG1yG1yTh1LeuSeMePro	180
Db	547	AACCGCTACCGGAGCCCGACGCTGTCTGCCAGGGCCCGGGGGGACCTCAAGCATGCC	606
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QY	201	ValPhe1leG1y1LeaAaPaPLeuG1u1ySeG1uG1yA1aPheVal1ySe1aSPH1aSeR	220
Db	667	GTCCTCATCGGCATCAACGACCTGGAGAGAGGGCGCTTCGTACTTGACCACTCC	726
QY	221	ProMeAr1aRG1yThSe1n1ySTTPAaSeRG1yG1uPProAaPaPa1a1yAaG1uG1u	240
Db	727	CCCATCGGACCTTCAACAAGTGGCGGACCGGTGAGCCCAACAAAGCTTACGAGAGAG	786
QY	241	AaPCySeValG1uMe1yVal1aSeRG1yG1yTPAaPaPa1a1aCySe1eThThMeT	260
Db	787	GACTGCGTGAAGATGGTGGCTTCGGCGGCTGMAACGACGTGGCTGCCAACACATG	846
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RESULT 8
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Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottfredsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C15
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	2,98e-269	Length:	1238
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-806-277A-6 (1-271) x US-09-991-073-356 (1-1238)

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Qy 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40

Db 127 CCATTGACATCTCTCAAGCCGCTGCGATGACGCTTGTCTGTCAAGTCTCTCTCTCT 186  
Qy 41 G1yleuLysg1yAspAlaG1yG1ulLysg1yAspLysg1yAlaProG1yArgProG1yArg 60  
Db 187 GGCCTCAAGGGGATGCGGAGAGAAAGGAGACAAAGGGCCCGCGAGCGGCTTGAGGA 246  
Qy 61 ValG1yProThrG1yG1ulLysg1yAspMetG1yAspLysg1yG1ulLysg1ySerValG1y 80  
Db 247 GTCGGCCCAACGGGAGAAAGAGACATGGGGGCAAGGAGCAAGAGGCGCTGTGGGT 306  
Qy 81 ArgHsg1yLysIleG1yProIleG1ySerLysg1yG1ulLysg1yAspSerG1yAspIle 100  
Db 307 GGTCTGGAAGAAATGGTCCATTTGGCTTAAAGGTGAAGAGATTCGGGTACATA 366  
Qy 101 G1yProProG1yProAsnG1yG1ulProG1yLeuProG1yCysG1yCysSerG1nLeuArgLys 120  
Db 367 GGAACCCCTGGTCTTAATGAGAACAGGCTCCCATGTGAGTGACGACGCTGGCAG 426  
Qy 121 AlaIleG1yG1uMetAspAsnG1nValSerG1nLeuThrSerG1uLeuLysPheIleLys 140  
Db 427 GCCATCGGGAGATGACAAACAGGTCTCTCAGCTGACAGCAGCAGCTCAAGTTCAAG 486  
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Db 487 AATGCTGTGCGCGGTGTGGCGAGAGAGACAAAGATCTTCTGTGTGAGAGAGAG 546  
Qy 161 LysArgTyrAlaAspAlaG1nLeuSerCysG1nG1yArgG1yG1yThrLeuSerMetPro 180  
Db 547 AAGGCTACGGGAGAGCCCAAGCTGTCTGTCCAGGGCCCGGGGGGACCGCTGAGTGGCC 606  
Qy 181 LysAspG1uAlaAlaAsnG1yLeuMetAlaAlaTyrLeuAlaG1nG1yLeuAlaArg 200  
Db 607 AAGGACGGAGCTGCAATGGCTGTATGGCGCATCTGGCCCAAGCCGGCTGGCCCGT 666  
Qy 201 ValPheIleG1yIleAsnAspLeuG1uLysG1uG1yAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCACTGGCATCAAGCCTGSAAGAGAGGGCGGCTGTGTACTGTGACCATCTCC 726  
Qy 221 ProMetArgThrPheAsnLysArgTyrSerG1yG1uProAsnAsnAlaTyrAspG1uL 240  
Db 727 CCCATCGGAGCCTTCAACAAAGTGGCGAGCGGTGAGCCCAATGCGCTAGACAGAGAG 786  
Qy 241 AspCysValG1uMetValAlaSerG1yG1yTyrPheAsnArgValAlaCysHisThrThre 260  
Db 787 GACTCGCGGAGATGTGGCTCGGCGGCTGGAACGACGTGGCTGCACACACCATG 846  
Qy 261 TyrPheMetCysG1uPheAspLysG1uAsnMet 271  
Db 847 TACTTCATGTGTGAGTTGACAAAGAGACATG 879

RESULT 9  
US-09-990-442-356  
Sequence 356, Application US/09990442  
Patent No. US20020132252A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann  
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APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
CURRENT APPLICATION NUMBER: US/09/990,442  
PRIOR FILING DATE: 2001-11-14  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 2,986-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277a-6 (1-271) x US-09-990-442-356 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCATCTGGACATCTCAGCGCGCTGGCGGATGACGCTGCTGTGAGATGCTGCTCCT 186

QY 41 GlyLeuLeuGlyAspAlaGlyGlnGlyAspGlyGlyValAProGlyArgProGlyArg 60  
Db 187 GGCCTTAAGGGGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246

QY 61 ValGlyProThrGlyGlnGlyAspMetGlyAspGlyGlyGlnGlySerValGly 80  
Db 247 GTGGGCGCCACGGAG 306

QY 81 ArgHisGlyLeuIleGlyProIleGlySerIleGlyGlnGlyAspSerGlyAspIle 100  
Db 307 GTCATGAG 366

QY 101 GlyProGlyProAsnGlyGlnProGlyLeuProGlyCysSerGlnLeuArgGly 120  
Db 367 GAGCCCCCTGCTCTATGAG 426

QY 121 AlaIleGlyGlnMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIle 140  
Db 427 GCCATCGGGGAGATGAGACCAACAGAGTCTCTCAGCTGAGACCAAGAGTCAAGTCAAG 486



[illegible]



Qy 261 TyphMetCysGluPheAspIysGluLysMet 271  
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RESULT 11  
US-09-993-604-356  
Sequence 356, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-993-604-356 (1-1238)

QY 1 MetArgIyAenIeuaIaLeuValGlyValIeulIeSerIeuaIaPheIeUSeRleu 20

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QY 21 ProSeRgIyHIsProGInProAlaGlyAspAspAlaCySeSerValGInIleLeuValPro 40  
DB 127 CCATCTGACATCTCTGACCGCGGTGGGATGAGCGCTGCTGTGTGAGATCTCTGTCTCT 186  
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyValaProGlyAProGlyAArg 60  
DB 187 GGCCTCAAGGGATGGGAGAGAAAGGAGCAAAAGGCCCGCCGACCGCTGGAGA 246  
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DB 247 GTGGCCCAACGGAGAAAGAGACATGGGGACAAAGACAAAGACATGTGGGT 306  
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DB 307 CGTCATGAAATAATGGTCCCATTTGGCTTAAAGTGAAGAAAGATTCGGGTGACATA 366  
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DB 607 AAGAGAGAGCTGCCAATGGCCGATGGCCGATCTGCGCAAGCCGCGCTGGCCCT 666  
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QY 261 TyrPheMetCyGlyLysPheAspLysGlyLysMet 271  
DB 847 TACTTCATGTGTAGTTGACAAAGAGAAACATG 879

## RESULT 12

US-09-990-456-356  
Sequence 356, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Inc  
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 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C22  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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## Alignment Scores:

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Pred. No.: 2,98e-269      Length: 1238
Score: 271.00             Matches: 271
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                      Gaps: 0

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US-09-806-277A-6 (1-271) x US-09-990-456-356 (1-1238)

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QY 21 ProSeRgIyAIProGInProIaIGIYAaPaAaIaCySeSeVaIaIleUaIPro
DB 127 CCACTCTGGAATCTCTGAGCCGCTGGGATGACCCCTGCTGAGATCTCTGCTCT
QY 41 GIlYeuIySeGIYAaPaIaGIyGIUySeGIYAaPlySeGIYAIProGIYAIProGIYAIP
DB 187 GGCCTCAAGGAGATGCGGAGAGAAAGACAAAGCCGCCGAGCGCTGGAGAAGA
QY 61 ValGIyProThRgIyGIUySeGIYAaPMeGIYAaPlySeGIYGIUySeGIYSeVaIGIY
DB 247 GTGGGCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY 81 ArgHISeGIYyIleGIyProIleGIySeRISeGIYGIUySeGIYAaPSeRGIYAaP
DB 307 CGATATGAGAAAAATTGGCTCATTTGGCTCTTAAGGTGAGAAAGAGATTCGGGTGACATA
QY 101 GIlYProThRgIyProAeNGIyGIUyProGIYleUProCYSeGIYCySeSeGIUleUaIyS
DB 367 GAGACCCCTGCTCTAAATGAGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

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QY 121 AlalIeGIyIuMeChAaPaNGInVaISeRGIUleUThSeRGIUleUyIyPheIleIyS
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QY 141 AaPaIaVaIaIaGIyValaIaRgIyUThRgIySeRyIleIyRleUeUaIySgIuGIU
DB 487 AATGCTGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 161 LyAaRgIyRAlaAaPaIaGIUleUSeRyGIUyIyAaRgIyGIYThRleUSeRMeTPro
DB 547 AAGGCTACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY 181 LyAaRgIyUaIaIaAaNGIyIeUeUaIaIaIyIleUaIaGIyIleUaIaAaRg
DB 607 AAGGAGAGAGCTCCATAGGCTGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 201 ValPheIleGIyIleAaPaIeUgIyUySeGIYValaPheValIyRSeAaPHeISeR
DB 667 GTCTTCATCGGATCAACAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY 221 ProMeTaRgThRPhaenIySTPaRgSeRGIyGIUProAaPaIaIyAaPSeRGIU
DB 727 CCATGCGGAGCTTCAACAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY 241 AaPcyValaIuMeUeUaIaIaSeRGIyGIYThRPaAaPaIaIaCySeHISThRMeT
DB 787 GACTGCTGAGATGAGTGGCTGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY 261 TyRPhaMeCySgIuPheAaPlySgIuAaSeM 271
DB 847 TACTTCATGCTGATGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

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## RESULT 13

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US-09-989-721-356
Sequence 356, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyer, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritlsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCES: F2730P1055
CURRENT APPLICATION NUMBER: US/09/989,721
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311

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[illegible]

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PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 2,986-269 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-09-989-721-356 (1-1238)

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Qy 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCATCTGGACATCTCTACAGCCGGCTGGCATGACGCTGCTGTGCGAGATCTTGTGCTCT 186

Qy 41 GlyLeuysGlyAspAlaGlyGlyLeuysGlyAspysGlyAlaProGlyArgProGlyArg 60  
Db 187 GGCTCTCAAGGGGATGGCGGAG 246

Qy 61 ValGlyProThrGlyGlyLeuysGlyAspMetCysAspysGlyGlyLeuysGlySerValGly 80  
Db 247 GTCGGCCCGGAG 306

Qy 81 ArgHisGlyLeuysIleGlyProIleGlySerLeuysGlyLeuysGlyAspSerGlyAspIle 100  
Db 307 CGTATGGAAAAATTGGTCCATTGGCTTAAAGTGAGAGAGAGAGAGAGAGAGAGAGAG 366

Qy 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyCysSerGlnLeuArglys 120  
Db 367 GGAACCCCTGGTCTTAATGAG 426

Qy 121 AlaIleGlyLeuMetAspAsnGlnValSerGlnLeuThrSerGlyLeuysPheIleGlys 140  
Db 427 GCCATCGGGAG 486

Qy 141 AsnAlaValAlaGlyValArgGlyLeuThrGlySerLeuysIleTyrLeuLeuValysGlyGlu 160  
Db 487 AATCTGTCTGGCTGTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546

Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValArgGlyTyrThrLeuSerMetPro 180  
Db 547 AAGGCTAGAGGGGAG 606

Qy 181 LysArgGlyAlaAlaAsnGlyLeuMetAlaAlaTyrTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGAGACAGGCTGCAATGGCTATGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666

Qy 201 ValPheIleGlyIleAsnAspLeuGlyLeuysGlyValAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCATCGGACATCAAG 726

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Qy 261 TyrPheMetCysGlyPheAspLysGlyAsnMet 271  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Acids Encoded and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC20  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

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 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 9  
 Length: 1238  
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 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-09-806-277A-6 (1-271) X US-09-992-598-356 (1-1238)

[illegible]

APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumaas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE: Zhang, Zemin  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleot  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
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US-09-806-277A-6 (1-271) x US-09-989-293A-356 (1-1238)

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QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200
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DB 667 GTCTTCATCGGCATCAACAGACTGGAGAGAGGGCGCTTCGTGTACTGACCACTCC 726
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Job time : 640 secs

GenCore version 5.1.6  
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Run on: December 17, 2004, 08:55:20 ; Search time 632 Seconds  
(without alignments)  
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Title: US-09-806-277a-6

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1441	100.0	1238	9 US-09-989-722-356	Sequence 356, App
3	1441	100.0	1238	9 US-09-989-723-356	Sequence 356, App
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Sequence 45, Application US/10258105  
Publication No. US20030158382A1  
GENERAL INFORMATION:  
APPLICANT: Wakamiya et al.  
TITLE OF INVENTION: No. US20030158382A1 Collectin  
FILE REFERENCE: 19036/38785  
CURRENT APPLICATION NUMBER: US/10/258, 105  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: PCT/JP01/03468  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: JP 2000-120358  
PRIOR FILING DATE: 2000-04-21  
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SEQ ID NO 45  
LENGTH: 813  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-10-258-105-45

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US-09-806-277a-6 (1-271) x US-10-258-105-45 (1-813)

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## RESULT 2

US-09-989-722-356

; Sequence 356, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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 Db 127 CCATCTGGAACATCTCTCAAGCCGCTGGCGATACCCCTGCTGTGCAAGATCTGTCCCT 186  
 QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60  
 Db 187 GGCTCAAGAGGAGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
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Db 427 GCCATCGGGAGATGAGACACAGGTCTCTACGTCGACGACGAGCTCAAGTTTCATCAAG 486  
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Qy 261 TyrPheMetCysGlyPheAspIleGlyAsnMet 271  
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Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zheng, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
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PRIOR FILING DATE: 1998-07-09

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Query Match: 100.00% Indels: 0  
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Qy 261 TyrrhmetCysGluPheAspLygluAsnMet 271  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1G56  
CURRENT APPLICATION NUMBER: US/09/989, 279  
CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17





Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Aubin L.  
APPLICANT: Kijavik, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zenlin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-07	PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09	

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Oy	21	ProSerGGLyHisPProGlnProAlaGlyAspAspAlaCysSerValGlnIIeLeuValPro	40
Db	127	CCATCTGGAAATCTCTCAAGCCGGCTGGCGATGACGCTGCTGTGTCAATCTCTGTCCT	188
Oy	41	GLyLeuLysGLyAspAlaGlyIuLysGLyAspLysGLyAlaProGlyArgProGlyArg	60

Db	187	GACCTCAAAAGGGAGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGACGGCTCGAAGA	246
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QY	141	AsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValLysGluGlu	160
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QY	161	LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro	180
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QY	201	ValPheIleGlyIleAsnAspLeuGluIysGluGlyAlaPheValTyrSerAspHisSer	220
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QY	261	TyrPheMetCysGluPheAspLysGluLysMet 271	
Db	847	TACTTCATGTGTGAAGTTTGACAAAGAGAAACATG 879	

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-28  
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Alignment Scores:  
 Pred. No.: 6, 238-157 Length: 1238  
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 Query Match: 100.00% Indels: 0  
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US-09-806-277a-6 (1-271) x US-09-989-731-356 (1-1238)

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 67 ATGAGGGGGAATCTGGCCCTGGTGGCGTTCTTCAACAGCTTGCCCTTCTGTCATGCTG 126  
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 127 CCATCTGACATCTCTCAGCGGCTGCGCATGACGCTGCTGTCAGATCTCTGCTCCT 186  
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 427 GCCATCGGGGAGATGAGACACAGGTCTCTGCTGACGAGGAGGAGGAGGAGGAGGAGGAG 486  
 141 AsnAlaValAlaGlyValArgGlyThrGlnSerIleIleYrLeuLeuValIleGlyGln 160  
 487 AATGCTGTGCGCGGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546

161 LysArgTyrAlaAspAlaGlnLeuSerCyseGlnIYargGlyThrLeuSerMetPro 180  
 547 AAGGCTACGGGAGAGCCCAAGCTGTCTGCCAGGGGCGCGGAGGAGGAGGAGGAGGAGGAG 606  
 181 LysAspGlyAlaAlaAspGlyLeuMetAlaIleYrLeuAlaGlnIleGlyLeuAlaArg 200  
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 Sequence 356, Application US/09989732  
 Patent No. US20020123463A1  
 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deenoyers, Luc  
 APPLICANT: Baton, Dan L.  
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 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2730PIC57  
 CURRENT APPLICATION NUMBER: US/09/989, 732  
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 PRIOR FILING DATE: 1998-02-25  
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PRIOR APPLICATION NUMBER: 60/089600	PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089653	PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/089948	PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/089952	PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/090246	PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090252	PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090254	PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090349	PRIOR FILING DATE: 1998-06-23	PRIOR APPLICATION NUMBER: 60/090355	PRIOR FILING DATE: 1998-06-23	PRIOR APPLICATION NUMBER: 60/090429	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090431	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090435	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090444	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090445	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090472	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090535	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090540	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090542	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090557	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090676	PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090678	PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090690	PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090694	PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090655	PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090696	PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090682	PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/090683	PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/091360	PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091478	PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091544	PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091519	PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091626	PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091982  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	6,23e-157	Length:	1238
Score:	1441.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-806-277A-6 (1-271) x US-09-991-073-356 (1-1238)

QY 1 MetatgglYanleuAlaleuValglYallleuIleSerleuAlaPhleuSerleuLen 20  
Db 67 ATGAGGGGAATCTGCGCTGTGGCGCTTCTTAATCAGCGCTTCTGTCTACATGCTG 126  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	6,23e-157	Length:	1238
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Best Local Similarity:	100.00%	Mismatches:	0
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US-09-806-277a-6 (1-271) x US-09-990-442-356 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleValPro 40  
Db 127 CCATCTGGACATCTCAGCGCGGTGGCGATGAGCGCTGCTGTGTGAGATCTTCCT 186  
QY 41 GlyLeuIleGlyAspAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
Db 187 GGCCTAAAGGGGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80  
Db 247 GTGGGCCCCAGGAG 306  
QY 81 ArgHisGlyValLeuIleGlyProIleGlySerIleGlyGlyGlyGlyGlyGlyGly 100  
Db 307 GGTATGAGAAATTTGGTCCCATTTGCTTAAAGTGAGAGAGAGAGAGAGAGAGAGAG 366  
QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyGlySerGlyLeuAlaGly 120  
Db 367 GAGCCCCCTGGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
QY 121 AlaIleGlyIleMetAspAsnGlnValSerGlnLeuThrSerGlyLeuLeuYspHeile 140  
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Alignment Scores:

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US-09-806-277a-6 (1-271) x US-09-991-163-356 (1-1238)

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Qy 41 GlyLeuLeuGlyAspAlaGlyGlyGlyGlyAspLeuGlyValAspGlyArgProGlyArg 60  
 187 GGCCTCAAAAGGGATCGGAGAGAGAGAGACAAAGGGCCCCCGACGGCTTGAGAG 246

Qy 61 ValGlyProThrGlyGlyLeuGlyAspMetGlyAspLeuGlyGlnIleGlySerValGly 80  
 247 GTGGGCCCAACGGGAGAAAAGGAGACATGGGGACAAAGGACAGAAAGGCACTGGGT 306

Qy 81 ArgHisGlyLeuGlyIleGlyProIleGlySerLeuGlyGlyValAspSerGlyAspIle 100  
 307 CGTCATGAGAAAATTTGTCTCCATGCTCTAAAGGTGAGAAAGGAAATTCGGTGCATCA 366

Qy 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyCysSerGlnLeuArgVal 120  
 367 GAAACCCCTGGTCTAATGAGAACAGGCTTCCATGTGAGTGCAGCCAGCTGGCAG 426

Qy 121 AlaIleGlyLeuMetAspAsnGlnValSerGlnLeuThrSerGlnLeuValAspIleVal 140  
 427 GCCATCGGGAGATGAGCAACAGGTCTCTCAGCTGACAGCGAGCTCAAGTTCATCAAG 486

Qy 141 AsnAlaValAlaGlyValArgGlyThrGlyLeuValIleValLeuValValGlyGly 160  
 487 AATGCTGTGCGCGGTGTGGCAGAGAGGAGACCAATCTACTGCTGTGAGAGGAG 546

Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetPro 180  
 547 AAGCGTTACGGAGCGCCAGCTGTCTTCCAGGGCGGGGGGACCGCTGACAGTCCC 606

Qy 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
 607 AAGAGACGAGGCTGCCAATGGCTGATGGCGCATACCTGGCCCAAGCCGGCCCGT 666

Qy 201 ValPheIleGlyTyrLeuAspLeuGlyValGlyGlyValAlaPheValTyrSerAspHisSer 220  
 667 GTCTTCATCGCATCAACAGCTGAGAGAGAGGGGCGCTTGTGTACTGTACCACTCC 726

Qy 221 ProMetArgThrPheAsnLysTyrPargSerGlyGlyProAsnAspAlaTyrAspGlyGly 240  
 727 CCATCGCGAAGCTTCAACAGATGGCGGACGGTGTGAGCCCAACATGCTTACAGAGGAG 786

Qy 241 AspCysValGlyMetValAlaSerGlyGlyTyrPasnAspValAlaCysHisIleThrMet 260  
 787 GACTGGTGAAGATGGTGGCTCGGGCGGCTGAAAGAGAGTGGCTGCAACCAACAG 846

Oy 261 TyphemetCysgluPheAspIysGluAsnMet 271  
Db 847 TACTTCATGTGTGAGTTTGACAGAGAAACATG 879

RESULT 11  
US-09-993-604-356  
Sequence 356, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/065186  
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 PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
 Pred. No.: 6.23e-157 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
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US-09-806-277a-6 (1-271) x US-09-993-604-356 (1-1238)

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 Db 427 GCCATCGGGAGATGAG 486  
 QY 141 AsnAlaValAlaGlyYAspLeuGlyYAspLeuGlyYAspLeuGlyYAspLeuGlyYAspLeu 160  
 Db 487 AATGCTGTGCGCCGCTGCGAG 546  
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 US-09-990-456-356 Application US/09990456  
 Patent No. US20020137890A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary B.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.

APPLICANT: KJavin,Ivar J.  
APPLICANT: Napier,Mary A.  
APPLICANT: Pan,James  
APPLICANT: Paoni,Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumes, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P27301C22  
CURRENT APPLICATION NUMBER: US/09/990,456  
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PRIOR FILING DATE: 1998-07-09

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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-806-277a-6 (1-271) x US-09-990-456-356 (1-1238)

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Db 127 CCATCTGGAATCTCTCAAGCGGCTGGGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186  
Qy 41 GlyLeuLysGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 60  
Db 187 GGGCTCAAGGGGATGGGAG 246  
Qy 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyValGlyValGlyValGlyVal 80  
Db 247 GTGGGCCCCACGGAG 306  
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Db 307 CGTCATGAGAAATTTGGTCCATGGCTTAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366  
Qy 101 GlyProProGlyProAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 120  
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## RESULT 13

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Sequence 356, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Batton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltisen, Mary E.  
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APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guirney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC55  
CURRENT APPLICATION NUMBER: US/09/989,721  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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QY	21	ProSerGlyHisProGlnProAlaGlyAbpAraAlaCySerValGlnIleLeuValPro	40
Db	127	CCATCTGGACATCTCAGCCGGGTGGCGATGACGCTGCTGTGTCAATCTCGTCCCT	186
QY	41	GlyLeuLysGlyYaBpaAlaGlyGlyLysGlyYaBpLysGlyValAlaProGlyAixProGlyAix	60
Db	187	GGCCTCAAAAGGGATCGGGAGAGAAAGGAGACAAAGCGCCCCCGAGCGGCTTGAAAGA	246
QY	61	ValGlyProThrGlyGlyLysGlyYaBpMetGlyYaBpLysGlyGlnLysGlySerValGly	80
Db	247	GTGGGCCCCCAGGGAGAAAGAGACATGGGGGCAAAAGACAGAAAGCAGATGTGGGT	306
QY	81	ArgHisGlyLysArgIleGlyProIleGlySerLysGlyGlyLysGlyYaBpSerGlyAAspIle	100
Db	307	CGTCATGAGAAATTTGGTCTCCCATGTGCTTTAAAGTGAGAAAGAGATTTCCGTGACATA	366
QY	101	GlyProProGlyProAmsGlyGlyLysProGlyLeuProCysGlyCysSerGlnLeuArgLys	120
Db	367	GGAACCCCTGTGTCTTAATGAGAACACAGGCTCCCATGTGATGAGACGACACTGGCAG	426
QY	121	AlaIleGlyGlyLysLeuAAspAmsGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys	140
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QY	141	AspAlaValAlaGlyValArgGlnThrGlySerLysIleTyrLeuLeuValLysGlnLys	160
Db	487	AAAGCTGTGGCCGGTGTGGCGAGACGAGACCAAGTCTACTCTGTGTAAAGAGAGAG	546
QY	161	LysArgTyrAlaAAspAlaGlnLysSerCysGlnGlyArgGlyTyrThrLysSerMetPro	180
Db	547	AAGCGCTACGGGACCCCGACGCTGTCTTCAGGGCCCGGGGGGCAACGCTGACATGCC	606
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Db	607	AAAGGAGAGGCTGCCAATGGCCGTGATGGCCGATACCTGGCGCAAGCCGGGCTGGCCGT	666
QY	201	ValPheIleGlyTyrLeuAAspLeuGlnLysGlnGlyAlaPheValTyrSerAAspHisSer	220
Db	667	GTCTTCATCGGATCAACGACCTGGAGAAAGAGGGCGGCTTGTGTACTCTGACACTCC	726
QY	221	ProMetAixThrPheAmsLysTyrPArSerGlyGlyLysProAmsAraAlaTyrAAspGlnLys	240
Db	727	CCATGCGGACCTTCAACAAATGGGCGACGGGTGAGCCCAATGTGCTTCAAGAGAGAG	786

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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

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DB: 9 Gaps: 0

US-09-806-277a-6 (1-271) x US-09-992-598-356 (1-1238)

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Db 127 CCATCTGGACATCTCTCAAGCCGGCTGGGATGACCCCTGCTCTGAGATCTCTGCTCT 186

QY 41 GlyLeuYsgGlyAspAlaGlyGlnLeuYsgGlyAspYsgGlyAlaProGlyArgProGlyArg 60

Db 187 GGCCTCAAGGGGATGGGGAG 246

QY 61 ValGlyProThrGlyGlnYsgGlyAspMetGlyAspYsgGlyGlnYsgGlySerValGly 80

Db 247 GTGGGCCCCAGGAG 306

QY 81 ArgHisGlyYsgGlyGlyProGlyGlySerYsgGlyGlnYsgGlyAspSerGlyAspIle 100

Db 307 CGTATGAG 366

QY 101 GlyProProGlyProAsnGlyGlnProGlyLeuProCysGlyCysSerGlnLeuArgYsg 120

Db 367 GAGCCCTGCTGCTTATGAG 426

QY 121 AlaIleGlyGlnMetAspAsnGlnValSerGlnLeuThrSerGlnLeuYsgPheIleYsg 140

Db 427 GCGATCGGGAGATGAG 486

QY 141 AsnAlaValAlaGlyValArgGlnThrGlnSerYsgIleYsgLeuValYsgGlnGln 160

Db 487 AATGCTCTCCCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546

QY 161 LysArgYsgAlaAspAlaGlnLeuSerCysGlnGlyYsgGlyGlyThrLeuSerMetPro 180

Db 547 AAGCGCTACCGGAG 606

QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaYsgLeuAlaGlnAlaGlyLeuAlaArg 200

Db 607 AAGGACAGAGCTGCAATGAGCTGATGCGCGCATACCTGCGAGAGAGAGAGAGAGAG 666

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Db 667 GTCTTATCGGATCAAG 726

QY 221 ProMetArgThrPheAsnYsgTrpArgSerGlyGlnProAsnAsnAlaYsgAspGlnGln 240

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Db 787 GACTGCTGAGATGAGTGGGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846

QY 261 TyrPheMetCysGlnPheAspYsgIleAsnMet 271

Db 847 TACTTCAATGCTGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

RESULT 15

US-09-989-293A-356

Sequence 356, Application US/09989293A

Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kjaev, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P27301C66

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 DB 187 GGCCTCAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCGAGCGCTGGAAGA 246  
 QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
 DB 247 GTCCGCCCGACGGAGAAAGAGACATGGGGGACAAAGACAGAAAGAGATGTGGGT 306  
 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
 DB 307 CGTCATGGAAAAATTGGTCCCATTTGGCTTAAGGTGAAAGAGATTCCGGTGACATA 366

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DB 367 GGACCCCTGGTCTTAATGAGAACCAAGGCTCCCATGTGTGACAGCCAGCTGGCAAG 426  
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pb 427 GCCATCGGGAGATGAGAACCAAGTCTCTGACCTGACCAAGCTCAAGTTTCATCAAG 486  
QY 141 AsnAlaValAlaGlyValArgGlnThrGlnSerLysIleTyrLeuLeuValLysGlnGlu 160  
DB 487 AATGCTGTGCGCGGTGTGCGGAGAGCAAGATCTTACTGTGTGTAAGAGAGAG 546  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlnValArgLysIleTyrLeuSerMetPro 180  
DB 547 AAGCGCTACGGCGAGCGCCAGCTGTCTGTCCAGGGCGCGGGGGCACGCTGAGCATGCCC 606  
QY 181 LysAspGlnAlaAlaAenglyLeuMetValAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
DB 607 AAGAGCGAGGCTGCCAATGCTGTGATGCGCATTCCTGCGCAGAGCGCGCTGCCCCGT 666  
QY 201 ValPheIleGlyIleAsnAspLeuGlnLysGlnGlyAlaPheValTyrSerAspHisSer 220  
DB 667 GTCTTCATCGGCATCAACGACCTGAGAGAGAGGGCGCTTCGTGTACTGTGACCACTCC 726  
QY 221 ProMetArgThrPheAsnLysTyrArgSerGlyGlnProAsnAsnAlaTyrAspGlnGlu 240  
DB 727 CCCATGCGGACCTTCMAACAGTGGCGAGCGGTGAGCCCAATGCTTACGACGAGAGAG 786  
QY 241 AspCysValGlnMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrThrMet 260  
DB 787 GACTGCGTGGAGATGTGGCTCGGGCGGCTGGAAAGAGCTGGCTGCGCACACCAACCATG 846  
QY 261 TyrPheMetCysGlnPheAspLysGlnAsnMet 271  
DB 847 TACTTCATGTGTGAGTTGACAGAGAGAACATG 879

Search completed: December 17, 2004, 11:34:15  
Job time : 639 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 05:42:01 ; Search time 3865 seconds

(without alignments)  
2355.024 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 1441  
Sequence: 1 MRGNLALGVGLISLFLSL.....NDVACHTMTMPCFDEKEM 271

## Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODEL=frame+\_p2n\_model -DEV=xlp  
-Q=/cgn2.1/USPTO\_spool\_p/US09806277/runcat\_15122004\_101628\_29262/app\_query.fasta\_1.455  
-DB=EST -QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=aplo -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09806277@cgn\_1.1.6425@runcat\_15122004\_101628\_29262 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hcc:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est1:  
9: gb\_g982:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	1252	3	CR604552 full-length
2	1441	100.0	1397	3	CR612268 full-length
3	1397	96.9	894	5	BU147034 AGENCOURT
4	1384	96.0	1083	5	BK427124 BX427124
5	1353	93.9	1078	5	BK33394 BX33394
6	1331	92.4	1383	3	AK003121 Mus muscu
7	1306	90.6	962	5	BQ927000 AGENCOURT
8	1286	89.2	1150	3	CR599770 full-length
9	1124	78.0	834	7	CO398423 AGENCOURT

c	10	1102	76.5	1095	5	BX394893	BX394893
	11	1100	76.3	1015	5	BX394625	BX394625
	12	1098	76.2	823	4	B1198782	B1198782
c	13	1072	74.4	1071	5	BX394624	BX394624
	14	1067	74.0	788	4	BM547424	BM547424
	15	1032	71.5	723	4	BM547424	BM547424
	16	1030	71.5	723	4	BM547424	BM547424
	17	1021	70.9	1012	2	BE260904	BE260904
	18	1013	70.3	640	2	BE383325	BE383325
	19	1000	69.4	672	2	BE206254	BE206254
	20	987.5	68.5	683	2	BE382433	BE382433
	21	980	68.0	702	2	BE311185	BE311185
	22	962	66.8	715	2	BE313199	BE313199
	23	955.5	66.3	737	2	BE313410	BE313410
	24	955	66.3	644	2	BE262656	BE262656
	25	944	65.5	1000	4	B1198831	B1198831
	26	937	65.0	613	2	BE312666	BE312666
	27	933	64.7	767	2	BE260355	BE260355
	28	930	64.5	893	2	BF314316	BF314316
	29	930	64.5	916	2	BF316717	BF316717
	30	928	64.4	654	2	BE312923	BE312923
	31	913	63.4	769	2	BE312920	BE312920
	32	903.5	62.7	892	2	BE314275	BE314275
	33	902.5	62.6	728	2	BE260359	BE260359
	34	884	61.3	619	4	B1199068	B1199068
	35	881	61.1	626	2	BF316496	BF316496
	36	869	60.3	962	5	B0069775	B0069775
	37	862.5	59.9	878	4	B1197505	B1197505
	38	859	59.6	828	7	CR602638	CR602638
	39	858	59.5	697	2	BF317087	BF317087
	40	848	58.8	542	2	BE313758	BE313758
	41	836.5	58.0	851	6	CB993054	CB993054
	42	836	58.0	537	2	BE261686	BE261686
	43	834	57.9	538	2	BE312003	BE312003
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	45	823	57.1	525	2	BE261369	BE261369

## ALIGNMENTS

RESULT 1  
CR604552  
LOCUS CR604552 1252 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CSDDC024Y19 of Neuroblastoma Cot  
ACCESSION CR604552  
VERSION CR604552.1 GI:50485359  
KEYWORDS HTC; CNSLT; CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE Li W.B., Gruber C., Jesssee J. and Polayes D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1252)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry Cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
into the NotI and BclI sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
1..1252  
/organism="Homo sapiens"

ORIGIN

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DM08YL18"  
/tissue\_type="Neuroblastoma Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

## Alignment Scores:

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Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-806-277a-6 (1-271) x CR604552 (1-1252)

QY 1 MetAArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
DB 104 ATGAGGGGGAAATCTGGCCCTGCTGAGGCTTCTAATCAACCTCGCCCTTCTCACTGCTG 163  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 164 CCATCTGGACATCTCTCAAGCCGCTGCGCATGACGCTGCTCTGTCAGATCCTCGTCCCT 223  
QY 41 GlyLeuIleuysGlyAspAlaGlyGlyIleuysGlyAspIleuysGlyValProGlyArgProGlyArg 60  
DB 224 GGCTCTCAAGGGGATGCGGGAG 283  
QY 61 ValGlyProThrGlyGlyIleuysGlyAspMetGlyAspIleuysGlyIleuysGlySerValGly 80  
DB 284 GTCCGGCCCAACGGAG 343  
QY 81 ArgHisGlyIleuysGlyIleuysGlyProIleuysGlySerIleuysGlyIleuysGlyAspIle 100  
DB 344 CGTATGAGAGAAATTTGGTCCCATTTGGCTCTAAGGTGAGAGAGAGATTCGGTGACATA 403  
QY 101 GlyProProGlyProAsnGlyGlyIleuysGlyProGlyProGlyGlyCysSerGlnLeuArgLys 120  
DB 404 GGAACCCCTGCTCTAATGAG 463  
QY 121 AlaIleGlyIleuysGlyAspAsnGlnValSerGlnLeuThrSerGlnLeuIleuysGlyPheIle 140  
DB 464 GCCATCGGGAGATGAGACACAGGCTCTCTCACTGACGACGAGCTCAAGTTCATCAAG 523  
QY 141 AsnAlaValAlaGlyValArgGlyIleuysGlyIleuysGlyIleuysGlyValGlyGlyGly 160  
DB 524 AATGCTGTGCGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyIleuysGlyIleuysGlyMetPro 180  
DB 584 AAGGCTAAGCGGAG 643  
QY 181 LysAspGlyAlaAlaAsnGlyIleuysGlyAlaIleuysGlyIleuysGlyIleuysGlyArg 200  
DB 644 AAG 703  
QY 201 ValPheIleuysGlyIleuysGlyIleuysGlyIleuysGlyIleuysGlyIleuysGlyIle 220  
DB 704 GTCTTCATCGGAGATGAG 763  
QY 221 PrometArgTyrPheAsnIleuysGlyIleuysGlyIleuysGlyIleuysGlyIleuysGly 240  
DB 764 CCCATCGGAG 823  
QY 241 AspCysValGlyMetValAlaSerGlyIleuysGlyIleuysGlyIleuysGlyIleuysGly 260  
DB 824 GACTGCGGAGAGATGAG 883  
QY 261 TyrPheMetCysGlyIleuysGlyIleuysGlyIleuysGlyIleuysGlyIleuysGly 271  
DB 884 TACTTCATGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916

RESULT 2  
CR612268  
LOCUS  
DEFINITION  
full-length cDNA clone CS0DM08YL18 of Fetal Liver of Homo sapiens  
(human).

ACCESSION  
CR612268  
VERSION  
CR612268.1 GI:50493075  
KEYWORDS  
HTC; CNS/LT cDNA.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1397)  
L.I.W.B., Gruber,C., Jesssee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished  
JOURNAL  
TITLE  
AUTHORS  
REMARK  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1397)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
1. 1397

## FEATURES

## source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DM08YL18"  
/tissue\_type="Fetal liver"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.6e-124 Length: 1397  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-806-277a-6 (1-271) x CR612268 (1-1397)

QY 1 MetAArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
DB 92 ATGAGGGGGAAATCTGGCCCTGCTGAGGCTTCTAATCAACCTCGCCCTTCTCACTGCTG 151  
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 152 CCATCTGGACATCTCTCAAGCCGCTGCGCATGACGCTGCTCTGTCAGATCCTCGTCCCT 211  
QY 41 GlyLeuIleuysGlyAspAlaGlyGlyIleuysGlyAspIleuysGlyValProGlyArgProGlyArg 60  
DB 212 GGCTCTCAAGGGGATGCGGGAG 271  
QY 61 ValGlyProThrGlyGlyIleuysGlyAspMetGlyAspIleuysGlyIleuysGlyIleuysGly 80  
DB 272 GTCCGGCCCAACGGAG 331  
QY 81 ArgHisGlyIleuysGlyIleuysGlyProIleuysGlySerIleuysGlyIleuysGlyAspIle 100  
DB 332 CGTATGAGAGAAATTTGGTCCCATTTGGCTCTAAGGTGAGAGAGAGATTCGGTGACATA 391  
QY 101 GlyProProGlyProAsnGlyGlyIleuysGlyProGlyProGlyGlyCysSerGlnLeuArgLys 120  
DB 392 GGAACCCCTGCTCTAATGAG 451





RESULT 4  
 LOCUS BX427124 1083 bp mRNA linear EST 04-MAY-2004  
 DEFINITION BX427124 Homo sapiens FETAL LIVER Homo sapiens cDNA clone  
 CS0DM008Y118 5-PRIME, mRNA sequence.  
 ACCESSION BX427124  
 VERSION BX427124.2 GI:47002248  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1083)  
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 JOURNAL  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 This sequence belongs to sequence cluster 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?b=CS0DM008Y09Q1&c=1719.f.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DM008Y118"  
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 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.57e-119 Length: 1083  
 Score: 1384.00 Matches: 266  
 Percent Similarity: 98.15% Conservative: 0  
 Best Local Similarity: 98.15% Mismatches: 5  
 Query Match: 96.04% Indels: 1  
 DB: 5 Gaps: 0  
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 QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIeserLeuAlaPheLeuSerLeu 20  
 Db 92 ATGAGGGGGAATCTGGCCCTGCTGGGGCTTCTTAATCAAGCCCTGCTCTCACTG 151  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
 Db 152 CCATCTGGACATCTCTCAAGCCGCTGGCGCATACCGCTGCTCTGTGACAGATCTGTCCT 211  
 QY 41 GlyLeuIysGlyAspAlaGlyValGlyValAspIysGlyValProGlyArgProGlyArg 60  
 Db 212 GGCTCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271  
 QY 61 ValGlyProThrArgGlyGlyValGlyAspMetGlyAspIysGlyValGlyValGlyVal 80  
 Db 272 GTGGGCGCCACAGGAG 331  
 QY 81 ArgHisGlyValIleGlyProIleGlySerIysGlyValGlyValAspSerGlyAspIle 100

Db 332 CGTCATGAGAAAATTGGTCCCATTTGGCTTAAGAGTAGAAGAGATCCGCTGACATA 391  
 QY 101 GlyProProGlyProAngGlyValProGlyValProGlyValProGlyValProGlyVal 120  
 Db 392 GAGACCCCTGCTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451  
 QY 121 AlaIleGlyIleMetAspAngGlnValSerGlnLeuThrSerGlnLeuIysPheIleLys 140  
 Db 452 GCCATCGGGAGATGAGACACACAGGTCTCTCACTGACGACGACGACGACGACGACG 511  
 QY 141 AsnAlaValAlaGlyValArgGlyValThrGlySerIysIleTyrLeuLeuValIysGlyGlu 160  
 Db 512 AATGCTGTCCCGCTGCTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571  
 QY 161 LysArgTyrTrpAlaAspAlaGlnIleSerCysGlnGlyValArgGlyValIleThrLeuSerMetPro 180  
 Db 572 AAGGCTACCGGAG 631  
 QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
 Db 632 AAGGACAGAGCTCCATATGAGCTGATGCGCGCATACCTGCGGACAG-6GCTGGCCCT 690  
 QY 201 ValPheIleGlyIleAsnAspLeuGlyValGlyValAlaPheValIleThrAspPheSer 220  
 Db 691 GTCTTCATCGGATCAACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750  
 QY 221 ProMetArgThrPheAsnIleTyrArgSerGlyValProAsnAsnAlaTyrAspGluGlu 240  
 Db 751 CCATGCGGAGCTTCAACAGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810  
 QY 241 AspCysValGluMetValAlaSerGlyValTyrAsnAspValAlaCysHisThrThrMet 260  
 Db 811 GACTGCGTGAATGAGTGGCTGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870  
 QY 261 TyrPheMetCysGluPheAspIysGluAsnMet 271  
 Db 871 TACTTCATGTGTAGTTAKAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903  
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 LOCUS BX333394 1078 bp mRNA linear EST 07-APR-2004  
 DEFINITION BX333394 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 cDNA clone CS0DC024Y19 5-PRIME, mRNA sequence.  
 ACCESSION BX333394  
 VERSION BX333394.2 GI:46262347  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1078)  
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 JOURNAL  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?b=CS0DC024Y19&c=1719.f.  
 Location/Qualifiers  
 1. 1078  
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Db	265	CGTATGGAAAAATTGGTCCATTGGCTTAAGGTGAGAAAGAGATTCCGGTGA	CACTA	324	
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Db	335	GGAACCCCTGGCTTCCTAATGGAACAACAGGCTCCCATGTGAATGACAGCCAGCTGGCGAAG	384		
Qy	121	AlaIleGlyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuMetPheIleIys	140		
Db	385	GCCATCGGGGAGATGACACACCAAGTCTTCACTGACGACCGAGACTCAAGTTCATCAAG	444		
Qy	141	AsnAlaValAlaGlyValArgGluThrGlnSerIysIleTyrLeuLeuValIysGluGlu	160		
Db	445	AATGCTGTGCGCGGTGTGGCGACAGCGAGACCAAGTCACTCTGGTGAAGAGAGAG	504		
Qy	161	LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValArgGlyIleThrLeuSerMetPro	180		
Db	505	AAGCCCTACCGCGAGCGCCAGCTGTCTGCGACAGGCGCGGGGCAACGCTGACATGCCCC	564		
Qy	181	LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg	200		
Db	565	AAGACGAGAGGCTGCCATAGCGCTTATGGCCGATACCTGGCGCAACGCGGCTGGCCGCT	624		
Qy	201	ValPheIleGlyIleAsnAspLeuGlnIlyArgGluGlyAlaPheValTyrSerAspHiser	220		
Db	625	GCTTTCATCGGCATCAACGACCTGGAAGAGAGGAGCGCGCTTGTGTACTCTGAACCACTCC	684		
Qy	221	PrometArgThrPheAsnLysTyrPargSerGlyGluProAsnAsnAlaTyrAspGluGlu	240		
Db	685	CCCATGCCGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTACGACGAGAG	744		
Qy	241	AspCysValGluMetValAlaSerGlyGlyTyrPasnAspValAlaCysHisThrThyret	260		
Db	745	GACTGCGGTGAGATGTGGTGGCTCGGCGGCTGGAACGACGTGGCTCGCACACACATG	804		
Qy	261	TyrPheMetCysGluPheAspLysGluLeuMet	271		
Db	805	TACTTCATGTGTGAGTTTGACACAGAGAACATG	837		
REFERENCE	CO398423	834 bp	mRNA	linear	EST 01-JUL-2004
LOCUS	CO398423				
DEFINITION	AGENCOURT 27822626 NIH_MGC_252		Rattus norvegicus	cdna clone	
ACCESSION	CO398423				
VERSION	CO398423.1	GI:49580339			
KEYWORDS	EST.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (bases 1 to 834)				
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cga@b3-remail.nih.gov Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin cDNA Library Preparation: Express Genomic cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LHAM15348 row: d column: 17 High quality sequence stopt: 696.				
FEATURES	Location/Qualifiers				
SOURCE	1..834				

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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7307203"
/tissue_type="Ovary, strain - Norway Line3, Age8 weeks.
Tissue was snap-frozen adn transferred in -70C. RNase freee
for the entire procedure"
/lab_host="DH10B Tora"
/clone_id="NIH_MGC_252"
/note="Organ; Vector: pDONR 201; Site_1: NotI;
Site_2: NotI; RNA obtained from female ovariex animals at
8 wk old. Tissues were snap-frozen and kept at -80C for
two days before RNA extraction and purification
(Tri-reagent method). cDNA was primed using oligo-dT
primer: 5'-pactgattctcagatgcagccgccccc(17)25-3' and
cloned into the EcoRV/NotI sites of pExpress-1.
Site-selection >1.25kb resulted in an average insert size
of 1.7kb. This primary library is not normalized
(normalized library is NIH_MGC_252) note: this was constructed by
Express Genomics (Frederick, MD). Access: this is a NIH_MGC
library"

```

ORIGIN

Alignment Scores:	
Pred. No.:	4,35e-95
Score:	1124.00
Percent Similarity:	91.86%
Best Local Similarity:	85.27%
Query Match:	78.00%
DB:	7
Length:	834
Matches:	220
Conservative:	17
Mismatches:	17
Indels:	6
Gaps:	2

US-09-806-277A-6 (1-271) x CO398423 (1-834)

QY 18 SerLeuLeuProSerGlyH1sPProGlnProAlaGlyAspAspAlaCysSerValGlnIle 37

Db 1 TCCTCACTGCGCATCTGGATGTCCTCCACAGACAACACAGAGAGCGCTCTCCGTGCAATT 60

QY 38 LeuValProGlyLeuLeuGlyAspAlaGlyGlnLeuGlyAspLeuGlyAlaProGlyArg 57

Db 61 CTGTGTCCTCCGCGCTCAAAAGGGAGATTCCAGAGAAAGGAAACAAGAGCGCCCGACGCG 120

QY 58 ProGlyArgValGlyProThrTrgGlyGlnLeuGlyAspMetCysAspLeuGlyGlnLeuGly 77

Db 121 CCAAGGAAGACTCGCCCGCCACAGAGAAAAAGAGACATGGGAGACAAGAGGACAGAAAGGC 180

QY 78 SerValGlyArgHisGlyLeuGlyIleGlyProIleGlySerIleGlyGlnLeuGlyAspSer 97

Db 181 ACTGTGGGCGCCCATGAGAAAAATTGTGTCCTATTGGCGCCAAAGAGTGAAGAAAAAGAGATTCT 240

QY 98 GlyAspIleGlyProProGlyProAsnGlyGlnProGlyLeuProCysGlnCysSerGln 117

Db 241 GGTGACATCGAGCCCGCTGGTCCAGAGGAGAACTGTGATTCATGTGATGTCAGCGAG 300

QY 118 LeuArgGlyValAlaIleGlyGlnMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeu 137

Db 301 CTAGGAAAGGCTATTGGGAGAGATGATACACAGTCACTCACTGACCACTGGATGATAAA 360

QY 138 PheIleLeuAsnAlaValAlaGlyValArgGlnLeuThrGlnSerGlyIleTyrLeuLeuVal 157

Db 361 TTCAATAAAAAATCTGTGCTGTGTGTGTGCGGAGAACGAGACAGATCTACCTGTGCTG 420

QY 158 LysGlnGlnLeuArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeu 177

Db 421 AAGGAGGAGAAAGGGATGATGCAGATGCCAGCTGTCTCGCCAAAGCGGAGGACACACTG 480

QY 178 SerMetProLysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGly 197

Db 481 AGCATGCCCAAAACAGACAGGACCAATGGCTGTGATGCTTCATACACTGCGACACGCTGCG 540

QY 198 LeuAlaArgValPheIleGlyIleAsnAspLeuGlnLeuGlnGlyAlaPheValTyrSer 217

Db 541 CTGGCTGGGCTTCTATTGGCATCAATGACTGTGAGAGAGAAAGTGTCTTCGTGATCTCG 600



QY 218 Asph1SerPromeArGrThrPheasnlySTrPArSerGlyGluProAsnAsnAlaYr 237  
 Db 601 GACCGCTCCCTATGACACCTTCAACAATGCCACGAGAGCCAC-AACGCTTAT 659  
 QY 238 AepGluGluAepCyValGluMetValAlaSerGlyGlyTPAen-----AspVal 254  
 Db 660 GATGAGAGAGACTGTGTGAGATGTGTGAGCTCAGT-GGCTGGACGATGTGCTGCACATT 718  
 QY 255 AlaCyS---HrThThMetEyrThMetCyGluGluPheAplyGluAsnMet 271  
 Db 719 ACATGTACTCATGTGAGAGTGCACAGAGACTGTGAGNCAGACGGAACGNCCTC 772  
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 LOCUS BX394893 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 DEFINITION CDNA clone CS0DC024YP19 3-PRIME, mRNA sequence.  
 ACCESSION BX394893  
 VERSION BX394893.2 GI:46921106  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1095)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 13, 2003 this sequence version replaced gi:30628356.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by life technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdnas?CS0DC024CH1ONP1&c=1719.f.  
 FEATURES  
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 sites of the pCMVSPORT 6 vector. Library was normalized."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,06e-93 Length: 1095  
 Score: 1102.00 Matches: 236  
 Percent Similarity: 93.28% Conservative: 0  
 Best Local Similarity: 93.28% Mismatches: 16  
 Query Match: 76.47% Indels: 8  
 DB: 5 Gaps: 0  
 US-09-806-277a-6 (1-271) x BX394893 (1-1095)  
 QY 20 LeuPProSerGlyYH4ProGlnProAlaGlyAspAspAlaCySerValGlnIleuVal 39  
 Db 1042 CTGCCATCTGCA-CATCTCTAGCCGCTGC-GATGAGC-TGCTCTGTGCAAGATCTCTGTC 986  
 QY 40 ProGlyLeuLysGlyAspAlaGlyGlyGlyAspLysGlyAla-ProGlyAyrProG 59  
 Db 965 CTGGCCTCAAGAGGAGATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 926

QY 59 YArValGlyProThrGlyGlyLysMetGlyAspLysGlyGlyLysSerVal 79  
 Db 925 AAGAGTGGGCCCCCAGGAGT 866  
 QY 79 LGlyAyrGlyGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGly 99  
 Db 865 GGGTGTGATGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 806  
 QY 99 pLlGlyProProGlyProAsnGlyGlyProGlyLysProGlyLysSerGlnLysAr 119  
 Db 805 CATAGA-CCCCCTGCTCTTAATGAGAGACAGGCTCTCCATGATGATGAG-ACCAGCG 748  
 QY 119 GLyAlaIleGlyLysLysMetAspAsnGlnValSerGlnLysSerGlnLysPheI 139  
 Db 747 CAAGGCCATCGGAGTTCAT 688  
 QY 139 eLyAsnAlaValAlaGlyValAyrGlyLysGlyLysSerLysIleTyrIleuValLysG 159  
 Db 687 CAAGATGTCTGCTCCCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628  
 QY 159 uGlyLysAyrGlyTrpAlaAspAlaGlnLysSerCyGlyGlyValArgGlyGlyThrLysSer 179  
 Db 627 GKAGAGAG-TCAGCGAT 570  
 QY 179 tProLysAspGlyLysAlaAsnGlyLysMetAlaAlaTyrLeuAlaGlnAlaGlyLysAl 199  
 Db 569 GCCAAG 511  
 QY 199 AArValPheIleGlyLysAsnAspLysGlyLysGlyLysAlaPheValTyrSerAsp 219  
 Db 510 CCGTCTCTTCATCGGAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451  
 QY 219 sSerPromeArGrThrPheasnlySTrPArSerGlyGluProAsnAsnAlaYrAyr 239  
 Db 450 CTCCCCATGTGAG 391  
 QY 239 uGlyAspCyValGlyLysMetValAlaSerGlyGlyTyrAsnAspValAlaCySH1StrTh 259  
 Db 390 GAGAGAGCTGCTGAG 331  
 QY 259 tMetYrPheMetCyGluGluPheAplyGluAsnMet 271  
 Db 330 CATGTACTCATGTGAGAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294  
 RESULT 11  
 BX394625 1015 bp mRNA linear EST 01-MAY-2004  
 LOCUS BX394625 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 DEFINITION CDNA clone CS0DC018YD07 5-PRIME, mRNA sequence.  
 ACCESSION BX394625  
 VERSION BX394625.2 GI:46920154  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1015)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 13, 2003 this sequence version replaced gi:30628263.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by life technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdnas?CS0DC018CB04QP1&c=1719.f.







QY	Db	QY	Db	RESULT 14
249	GLVGLYTPAaagAaVAlACyBhIshThrTmTcTYrPhMeCtCyGGLnPhesApLys	269	GLuSsnMet 271	BF311981 788 bp mRNA linear EST 21-NOV-2000
381	GGCGGCTGAAACGACGTGGCTGCGACACACCACTGACTTCACTGTGAGTTTGACAAAG	321	GAGAACATG 313	60189783221 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4127454 5', mRNA sequence.
				BF311981
				BF311981.1 GI:11259754
				EST.
				Homo sapiens (human)
				Homo sapiens
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
				1 (bases 1 to 788)
				NIH-MGC http://mgc.nci.nih.gov/.
				National Institutes of Health, Mammalian Gene Collection (MGC)
				Unpublished (1999)
				Contact: Robert Strausberg, Ph.D.
				Email: cgsabbs-remail.nih.gov
				Tissue Procurement: ATCC
				CDNA Library Preparation: Ling Hong/Rubin Laboratory
				CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
				DNA Sequencing by: Incyte Genomics, Inc.
				Clone distribution: MGC clone distribution information can be
				found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov
				Plate: LNCMI018 row: 0 column: 07
				High quality sequence stop:703.

## FEATURES

### Source

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/mol_type="mrna"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 19"
/notes="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

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**ORIGIN**

### Alignment Scores:

Pred. No.:	8.93e-90	Length:	768
Score:	1067.00	Matches:	2240
Percent Similarity:	92.98%	Conservative:	1
Best Local Similarity:	92.56%	Mismatches:	12
Query Match:	74.05%	Indels:	7
DB:	2	Gaps:	1

US-09-806-277A-6 (1-271) x BF311981 (1-788)

QY 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20

Db 75 ATGAGGGGAATCTGGCCCTGGTGGCGTTCTATCAGCCTGGCCTTCCTGTCACTGCTG 134

21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40

Db 135 CCATCTGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCT 19

41 G L Y L e u L y S G L Y A B P A I a G L Y G L u L y S G L Y A B P L y S G L Y A L a P r o G I Y a r g P r o G I Y a r g 60

Db	195	GGCCTCMAAAGGAGATCGCGGAGAGAAAGGAGACMAAAGCGCCCGGACGCGCTGGAA	254
OY	61	ValGlyProThrGlyGlyIuLysGlyYAspMetGlyAspLysGlyGluLysGlySerValGly	80
Db	255	GTCGGCCCCCAGGGAGAAAAAGAGACATGGGGGACMAAAGGACAAAGGCGAGTGGGT	314
OY	81	ArgHisGlyLysIleGlyProIleGlySerLysGlyGluLysGlyYAspSerGlyAspIle	100
Db	315	GCTCATGGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGTGACATA	374
OY	101	GlyProProGlyProAsnGlyGluProGlyLeuProCysGluCysSerGluLeuAsnArgLys	120
Db	375	GGACCCCTCGTCTCTAATGAGAGAACGAGCTCCCATATGATGACAGCCAGCTGGCCAA	434
OY	121	AlaIleGlyIuMetAspAsnGlnValSerGlnLeuThrSerGluLeuLysAspIleLys	140
Db	435	GCCATCGGGAGATGAGCAACCAAGGTCTCTCAGCTGACCAAGGAGCTCAAGTTTCATCA	494
OY	141	AsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValLysGlu	160
Db	495	AATCTGTGCGCGGTGTGTGGGAGACGGAGAGCAAGATCTACCTGGTGTGAAGAGGGA	554
OY	160	uLysArgCysAlaAspAlaGlnLeuSerCysGlnGlyValArgGlyGlyThrLeuSerMetPr	180
Db	555	GAAAGCGTACCGCGAGCGCCACGCTGCTCTGCCAGGGCCCGGGGGCAAGCTAGCATGCC	614
OY	180	oLys-AspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaA	200
Db	615	CAAAGTACGAAGCTCGCAATGGCTGATGGCGCATTACTGGCGCAAGCGCGGCTGGGCG	674
OY	200	rgValPheIle-GlyIleAsnAspLeuGluLys-GluGlyAlaPheValTyrSerAspHi	219
Db	675	GTCGCTTCATCGGGCATCAACGACTTGAGAAAGGAGGGCGCTTCGTGTAACTGACCA	734
OY	219	sSerProMetArgThrPheAsnLysTrpArgSerGlyGluProAsnAlaAlaTyrAsp	238
Db	735	ATCCCCATGGCGAC-CTTCAAGATGGCGAC-GGTAGCA--AAATGCTTACGAC	786

## RESULT 15

BM547424

LOCUS

DEFINITION

**ACCESSION**

**VERSION**

## KEYWORDS

**SOURCE**  
**ORGANIS**

0  
1  
2  
3  
4  
5  
6  
7  
8  
9

## REFERENCE

**AUTHORS**  
**TITLE**

JOURNAL

COMMENT

## FEATURES

**Sour**

/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;  
 Site 1: ECoRV (destroyed); Site 2: NotI; RNA source pool  
 of three ovaries, from females ranging in age from 38 to  
 49 yo. Library is oligo-dT primed and directionally cloned  
 (ECoRV site is destroyed upon cloning). Average insert  
 size 2.1 kb, insert size range 1-3.5 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 036."

## ORIGIN

## Alignment Scores:

Prod. No.:	2.57e-86	Length:	1094
Score:	1032.00	Matches:	235
Percent Similarity:	72.11%	Conservative:	8
Best Local Similarity:	69.73%	Mismatches:	17
Query Match:	71.62%	Indels:	77
DB:	4	Gaps:	3

US-09-806-277a-6 (1-271) x BMS47424 (1-1094)

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QY      21 ProSerGlyHisProGlyProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40
DB      102 CCAATGTGAACATCTCAAGCCGCTGGCTGCGATGACGCTTGTGTGCAAGATCTCTGTCCT 161
QY      41 GlyLeuLysGlyAspAlaGlyValGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60
DB      162 GGCCTCAAAAGGGGATGCGGAGAGAAAGGAGACAAAGGGGCCCCCGGACGGCTGTGAAGA 221
QY      61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysGlySerValGly 80
DB      222 GTGGCCCCACGCGGAGAAAGAGACATGGGGGACAAAGGACAGAAAGCGCATGTGGGT 281
QY      81 ArgHisGlyLysIleGlyProIleGlySerLysGlyLysGlyAspSerGlyAspIle 100
DB      282 CGTCTATGAAAAAATTTGCTCCATTTGGCTTTAAAGGTGAGAAAGAGATTCCGGTACATA 341
QY      101 GlyProProGlyProAsnGlyGlyPro----- 109
DB      342 GGAACCCCTGGTCTTAATGAGAACACAGTCTTGGGACCGCAGATGAGAGAGAACG 401
QY      109 ----- 109
DB      402 GCTGCTTGAAGGTGTGCTTGGCTGCTGATCTTGCTGAGTGTGATGCGCTGAGATCAG 461
QY      109 ----- 109
DB      462 TGTCACTGACTGGCCGAGACGATCCGCTCAGGGGCACTCCAGGCACTCAGCCAACTGA 521
QY      110 ----- 110
DB      522 GGGGGCCGGAGCAAAAGCTCTGTGGGAGACAGAAAGACCTGGAAGGCTCCCATGTGATGCAG 581
QY      116 TGIleuLysGlyValAlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlyLe 136
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QY      136 ulysPheIleLysAsnAlaValAlaGlyValArgLysThrGlySerLysIleTyrLeuLe 156
DB      642 CAAGTTCAATCAAGATGCTGTGCGCGGTGTGCGCAGACGAGAGCAAGATCTTACTGCT 701
QY      156 uValLysGlyLysGlyValArgTyrAlaAspAlaGlnLeuSer--CysGlnGlyArg--GlyGly 175
DB      702 GGTGAAGAGAGAAACCTACGCGGACGCCCAAGCTGTCTTGGCCAGGCCCCGGGGGGGC 761
QY      176 ThrLeuSerMetProLysAspGlyLysAlaAlaAsnGlyLeuMetAlaIleTyrLeuAla--G 195
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QY      195 nAlaGlyLeu-AlaArgValPheIleGlyIleAsnAspLeuGlyLysGlyValAla-Phe 214
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QY      215 ValLysSer-AspHisSerProMetArgThrPheAsnLysTrp--ArgSerGlyGlyPr 233
DB      882 CGTACTCTGAGACCATCTCCCATGCGGAACTTCACAAATGGGGCGCAACGGGGGAAACC 941
QY      233 oAsnAsnAlaLysr--AspGlyLysProCysValGlu--MetValAlaSerGlyGly-Tr 251
DB      942 CACCAATGCTATGACACCAAGAGAAATGCTGTGCAAAATGTGGGCTTGGGCGGCTTG 1001
QY      251 PAsn-AspValAlaCysHisThrThrMet 260
DB      1002 GAACAAAGGGGCTTGGCCCAACACGATG 1030

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Search completed: December 17, 2004, 09:59:53  
 Job time : 3874 secs

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[illegible]

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AX403469			
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DEFINITION	Sequence	356 from Patent WO0073454.	linear
ACCESSION	AX403469		

VERSION	AX403469.1	GI:21436970
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
AUTHORS	1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Denoyers, L., Eaton, D., Ferrara, N., Gerber, H., Gertulis, M., Goddard, A., Godowski, P., Grimaldi, C.J., Guiney, A.L., Kijavits, I., Napier, M.A., Pan, J., Paoletti, N.F., Roy, M., Stewart, T.A., Tunes, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.	
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL	Patent: WO 0073454-A 356 07-DEC-2000;	
FEATURES	Genentech Inc. (US)	
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Best Local Similarity	100.0%	Pred. No. 0;
Matches 1230; Conservative	0; Mismatches	0; Indels 0; Gaps 0
QY	24	GCGACGGGCGACGAGCGCCCGCTTGGCTTACGGCTGACGAGTTGGTCTTGGCTTGGC 83
DB	1	GCGACGGGCGACGAGCGCCCGCTTGGCTTACGGCTGACGAGTTGGTCTTGGCTTGGC 60
QY	84	CTCAGAGATGAGGGGGAATCTGAGCCCTGCTGGGCGCTTCAATACGCTGGCTTCTGTC 143
DB	61	CTCAGAGATGAGGGGGAATCTGAGCCCTGCTGGGCGCTTCAATACGCTGGCTTCTGTC 120
QY	144	CTGCTGCGCATCTGGAATCTCTACGCGGCTGGCGATGACGCTGCTCTGTGCGAATCTTC 203
DB	121	CTGCTGCGCATCTGGAATCTCTACGCGGCTGGCGATGACGCTGCTCTGTGCGAATCTTC 180
QY	204	GTCCCTGGCTCAAAAGGGGATGCGGGAAGAAAGGGAGCAAAAGGCGCCCGGACGGGCTT 263
DB	181	GTCCCTGGCTCAAAAGGGGATGCGGGAAGAAAGGGAGCAAAAGGCGCCCGGACGGGCTT 240
QY	264	GGAAGAGTCTGGCGCCCGGACGGGAGAAAGAGAGCATGCGGGGACAAAGACAGAAAGCACT 323
DB	241	GGAAGAGTCTGGCGCCCGGACGGGAGAAAGAGAGCATGCGGGGACAAAGACAGAAAGCACT 300
QY	324	GTGGGTCTGTCATGGAATAATTGGTCCCATTTGGCTCTAAAGGTGAAGAAAGAAATTCGGT 383
DB	301	GTGGGTCTGTCATGGAATAATTGGTCCCATTTGGCTCTAAAGGTGAAGAAAGAAATTCGGT 360
QY	384	GACATAGAGACCCCTGCTGCTTAATGAGAACCGAGGCTTCCCATGTAATGTCAGCCAGCTG 443
DB	361	GACATAGAGACCCCTGCTGCTTAATGAGAACCGAGGCTTCCCATGTAATGTCAGCCAGCTG 420
QY	444	CGCAAGGCTCATCGGGAGATGAGAACCAAGGTTCTTCACTGACCTGACGAGCTCAAGTTTC 503
DB	421	CGCAAGGCTCATCGGGAGATGAGAACCAAGGTTCTTCACTGACCTGACGAGCTCAAGTTTC 480
QY	504	ATCAAGAAATGCTGTGCGCGGTGTGGTGGGAGACGGAGACCAAGATTTACTGCTGGTAGAG 563
DB	481	ATCAAGAAATGCTGTGCGCGGTGTGGTGGGAGACGGAGACCAAGATTTACTGCTGGTAGAG 540
QY	564	GAGGAGAAACGCTTACGCGGACGCCAGGCTGCTTGGCCAGGGCCGCGGGGGCAACGCTGAC 623
DB	541	GAGGAGAAACGCTTACGCGGACGCCAGGCTGCTTGGCCAGGGCCGCGGGGGCAACGCTGAC 600
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VERSION  
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REFERENCE  
AUTHORS 1 Baker, K.P., Ferrara, N., Gerber, H., Gerltzen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoletti, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 167 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerltzen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
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Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, B., Sanchez, C., Schoenfeld, J., Seashagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vages, A., Vandien, R., Watanabe, C., Wiand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, M.I., and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL  
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Clark, H.F.  
Direct Submission  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Query Match 98.2%; Score 1230; DB 9; Length 1238;  
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Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schreier, T.E., Brownstein, M.J., Udén, T.B., Toishiyaki, S., Caramici, P., Prange, C., Raha, S.S., Loguigiano, N.A., Peters, G.J., Abramson, R.D., Mullighy, S.J., Bosak, S.A., McEwan, P.J., McCormann, K.U., Malek, U.A., Gunaratne, P.H., Richards, S., Wooley, K.C., Hale, S., Garcia, A.W., Gay, L.J., Hilly, S.W., Vialation, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Keltman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzyzanski, M.I., Skalka, U., Smalins, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16939-16903 (2002)

12477932

2 (bases 1 to 1248)

Straubberg, R.

Direct Submission

Submitted (03-NOV-2000) National Institutes of Health, Mammalian

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DEFINITION Novel collection.  
ACCESSION BD103303  
VERSION BD103303.1 GI:22648877  
KEYWORDS MO 0181401-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 1139)  
TITLE Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
JOURNAL Novel collection  
Parent: MO 0181401-A 2 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI

COMMENT	OS	Homo sapiens (human)
PN	MO 0181401-A/2	
PD	01-NOV-2001	
PF	23-APR-2001 WO 2001JP003468	
PR	21-APR-2000 JP 00P 120358	
PI	NOBUTAKA WAKAMITSU, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI SAKAMOTO,	
PI	YUICHIRO KISHI	
PC	C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53	
CC	Novel collection	
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ORIGIN		
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D6		1031	GCCATGCTTAAAGGAGAAAATGAAGAAGTTCCTGTGGGGTGCAGTCTTGAAGAACAGAGT	1090
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ACCESSION			BC009951	
VERSION			BC009951.2	
KEYWORDS			WGC.	
SOURCE			Homo sapiens (human)	
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE			Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS			1 (bases 1 to 1417)	
			Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L., Scheer,T.E., Brownstein,M.J., Udell,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullenhy,S.U., Boeck,S.A., McKean,P.J., McKeown,R.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wozley,K.C., Hale,S., Garcia,A.M., Gay,U.J., Holly,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schnut,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalka,U., Smalund,D.B., Scherch,A., Schein,J.E., Jones,S.J., and Marra,M.A.	
TITLE			Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL			Proc. Natl. Acad. Sci. U.S.A.	
PUBMED			12477932	
REFERENCE			2 (bases 1 to 1417)	
AUTHORS			Strausberg,R.	
TITLE			Direct Submission	
JOURNAL			Submitted (02-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK			NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT			On Aug 19, 2003 this sequence version replaced gi:14714411. Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov	
			Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Grante,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R.,	

Maduro, Q. L., Mastello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Stanirip, S., Thomas, P. J., Touchman, J. W., Taurgeon, C., Vogt, J. L., Walker, M. A., Weherby, K. D., Wiggins, L., Young, A., Zhang, L., H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILM, at: <http://image.llnl.gov> Series: IRL, Plate: 20 Row: f Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

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source

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## CDS

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
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LOCUS BD103330  
DEFINITION Novel collectin.  
ACCESSION BD103330.1 GI:22648904  
VERSION WO 0181401-A/29.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1269)  
AUTHORS Wakamiya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.  
TITLES Novel collectin  
JOURNAL Patent: WO 0181401-A-29 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/29  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	(bases 1 to 1067)		
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	PIUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI			
	KESHI, KATSUKI OTANI, TAKASHI SAWAMOTO, YUICHIRO KISHI			
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QY	770 GTGGGCGCAGCGGTGAGCCCAACATAGCTTACGACAGAGAGAGCTGGGTGAGATGATGTCG	829		
DB	671 GTGGGCGCAGCGGTGAGCCCAACATAGCTTACGACAGAGAGAGCTGGGTGAGATGATGTCG	730		
QY	830 CTCGGGCGGCTGGAACGAGCTGAGCTGCGCAACCAACATGTAATCTCATGTGAGTTGA	889		
DB	731 CTCGGGCGGCTGGAACGAGCTGAGCTGCGCAACCAACATGTAATCTCATGTGAGTTGA	790		
QY	890 CAAGAGAACATGTAGGCTCTAGGCTGGGGCTGCCATTGGGGGCCCAATGTCCTTCG	949		
DB	791 CAAGAGAACATGTAGGCTCTAGGCTGGGGCTGCCATTGGGGGCCCAATGTCCTTCG	850		



QY 950 AGGGTTGGCAGGAGCAGAGCCAGCCATGTCGAGCAGGAGACTGTCCTCTGTGAA 1009  
DB 851 AGGGTTGGCAGGAGCAGAGCCAGCCATGTCGAGCAGGAGACTGTCCTCTGTGAA 910  
QY 1010 GGGTGGAGGCTCACTGATAGAGGAGGCTGTGTCTAACTGAGAAATAGGCTATCTTAA 1069  
DB 911 GGGTGGAGGCTCACTGATAGAGGAGGCTGTGTCTAACTGAGAAATAGGCTATCTTAA 970  
QY 1070 GAGGAAATGAAAGTGTCTCTGGGGTGTCTGTCTGAAAGAGCAGATTTCATTA 1129  
DB 971 GAGGAAATGAAAGTGTCTCTGGGGTGTCTGTCTGAAAGAGCAGATTTCATTA 1030  
QY 1130 ATTGTAGCCCAATGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1166  
DB 1031 ATTGTAGCCCAATGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1067

RESULT 12  
BD103332  
LOCUS BD103332 813 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel collectin.  
ACCESSION BD103332  
VERSION BD103332.1 GI:22648906  
KEYWORDS WO 0181401-A/31.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 31 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PN WO 0181401-A/31  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collectin  
FH Key  
FT source  
FT Location/Qualifiers  
1. 813  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="caxon:9606"

FEATURES  
Source  
1. 813  
Location/Qualifiers  
1. 813  
/organism="Homo sapiens (human)".

ORIGIN  
Query Match 64.9%; Score 813; DB 6; Length 813;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 ATGAGGGGAAATCTGGCCCTGGGGCGCTTCAATCAGGCTGGCCCTCTGCTCACTGCTG 149  
DB 1 ATGAGGGGAAATCTGGCCCTGGGGCGCTTCAATCAGGCTGGCCCTCTGCTCACTGCTG 60  
QY 150 CCATCTGAGCATCTCAGCCGGCTGGCGATGACGGCTGTCTGTGCAATCTCTCTCCCT 209  
DB 61 CCATCTGAGCATCTCAGCCGGCTGGCGATGACGGCTGTCTGTGCAATCTCTCTCCCT 120  
QY 210 GGCCTCAAAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGGCTTGAAGA 269  
DB 121 GGCCTCAAAAGGGGATGCGGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGGCTTGAAGA 180  
QY 270 GTCCGCCCAACGGAGAAAGAGAGCATGGGGGCAAAAGAGCAGAAAGGAGCTGTGGGT 329

DB 181 GTCCGCCCAACGGAGAAAGAGAGCATGGGGGCAAAAGAGCAGAAAGGAGCTGTGGGT 240  
QY 330 CGTATGAAATAATTTGTTCCCATTTGGCTCTAAAGTGAAAGAGATTTCCGGTGACATA 389  
DB 241 CGTATGAAATAATTTGTTCCCATTTGGCTCTAAAGTGAAAGAGATTTCCGGTGACATA 300  
QY 390 GGACCCCTGGTCTCTAAATGAGAAACAGGCTCTCCCATGTAGTGAGGACGACCTGGCAAG 449  
DB 301 GGACCCCTGGTCTCTAAATGAGAAACAGGCTCTCCCATGTAGTGAGGACGACCTGGCAAG 360  
QY 450 GCCATCGGGAGATGAGCAACAGAGTCTCTCAGCTGACACAGCAGCTCAAGTTCAATCAAG 509  
DB 361 GCCATCGGGAGATGAGCAACAGAGTCTCTCAGCTGACACAGCAGCTCAAGTTCAATCAAG 420  
QY 510 AATGCTGTCCCGGTGTGCGGAGACGGAGACCAAGATCTTCTGTGTGTGAGAGAGAG 569  
DB 421 AATGCTGTCCCGGTGTGCGGAGACGGAGACCAAGATCTTCTGTGTGTGAGAGAGAG 480  
QY 570 AAGGCTACGCGGAGACGCCAGCTGTCTCTGCGCAGGGGCGGGGGGACGCTGAGCATGCCC 629  
DB 481 AAGGCTACGCGGAGACGCCAGCTGTCTCTGCGCAGGGGCGGGGGGACGCTGAGCATGCCC 540  
QY 630 AAGGAGAGGCTGCGCAATGAGCTGATGAGCGCATACCTGCGCAAGCCGAGCTGGCCGT 689  
DB 541 AAGGAGAGGCTGCGCAATGAGCTGATGAGCGCATACCTGCGCAAGCCGAGCTGGCCGT 600  
QY 690 GTCTTCATCGGCATCAACAGACCTGAGAGAGAGGAGGCGCTTGTGTACTTGACCACTCC 749  
DB 601 GTCTTCATCGGCATCAACAGACCTGAGAGAGAGGAGGCGCTTGTGTACTTGACCACTCC 660  
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DB 661 CCATGCGGAGACCTTCAACAGATGGGCGAGCGGTGAGCCCAATGCTCTGACAGAGAGAG 720  
QY 810 GACTGCGTGAAGATGATGAGCTCGGCGGCTGGAACGAGCTGAGCTGCGCACACCATG 869  
DB 721 GACTGCGTGAAGATGATGAGCTCGGCGGCTGGAACGAGCTGAGCTGCGCACACCATG 780  
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DB 781 TACTTCATGTGTGAGTTGACAGAGAGACATG 813

RESULT 13  
BD103306  
LOCUS BD103306 1067 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel collectin.  
ACCESSION BD103306  
VERSION BD103306.1 GI:22648880  
KEYWORDS WO 0181401-A/5.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1067)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 5 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PN WO 0181401-A/5  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collectin  
FH Key  
FT CDS  
FT Location/Qualifiers  
1(41)..(803).

FEATURES  
Location/Qualifiers  
1(41)..(803).

## SOURCE

1. 1067  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 64.4%; Score 807; DB 6; Length 1067;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 807; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 AAAGGTGAGAAAGAGATTCGGTGAACATAGACCCCTGGTCTTAATGAGAAACAGGC 419  
DB 261 AAAGGTGAGAAAGAGATTCGGTGAACATAGACCCCTGGTCTTAATGAGAAACAGGC 320  
QY 420 CTCCCATGTGATGACAGCACTGGGCAAGCCATCGGGAGATGAGAACACAGGTCTCT 479  
DB 321 CTCCCATGTGATGACAGCACTGGGCAAGCCATCGGGAGATGAGAACACAGGTCTCT 380  
QY 480 CAGGTGACACGAGCTCAAGTTCTCAAGATGCTGCGCGGTGTCGCGAGACGAG 539  
DB 381 CAGGTGACACGAGCTCAAGTTCTCAAGATGCTGCGCGGTGTCGCGAGACGAG 440  
QY 540 AGCAAGATCTACCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599  
DB 441 AGCAAGATCTACCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500  
QY 600 CAGGGCCCGGGGGGAG 659  
DB 501 CAGGGCCCGGGGGGAG 560  
QY 660 GCATACCTGCGGCAAGCGGCTGGCCCGGTCTTTCATCGGCATCAACGACTGTGAGAG 719  
DB 561 GCATACCTGCGGCAAGCGGCTGGCCCGGTCTTTCATCGGCATCAACGACTGTGAGAG 620  
QY 720 GAGGGCGGCTTGTGTACTCTGACCACTTCCCATGCGGACCTTCAACAGTGGCGAGC 779  
DB 621 GAGGGCGGCTTGTGTACTCTGACCACTTCCCATGCGGACCTTCAACAGTGGCGAGC 680  
QY 780 GGTGAGCCCAACAGCTGAG 839  
DB 681 GGTGAGCCCAACAGCTGAG 740  
QY 840 TGGAAAG 899  
DB 741 TGGAAAG 800  
QY 900 ATGTGAGCTTCAAGCTGAG 959  
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QY 1080 AAAGGTTCCTGGGCTGCTGCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1139  
DB 981 AAAGGTTCCTGGGCTGCTGCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040  
QY 1140 CAATGTCAATTATTAATTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1166  
DB 1041 CAATGTCAATTATTAATTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1067

RESULT 14  
LOCUS BD103329 1197 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel collectin.  
ACCESSION BD103329  
VERSION BD103329.1 GI:22648903

## KEYWORDS

MO 0181401-A/28.  
SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 1197)

## AUTHORS

Wakamiya,N., Keshi,H., Ocani,K., Sakamoto,T. and Kishi,Y.

## TITLE

Novel collectin

## JOURNAL

Patent: WO 0181401-A 28 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI

## COMMENT

OS Homo sapiens (human)  
PN MO 0181401-A/28  
PP 01-NOV-2001  
PP 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
CC Novel collectin  
FH Key location/Qualifiers  
FT CDS (265)..(933).

## FEATURES

## SOURCE

1. 1197  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 64.4%; Score 807; DB 6; Length 1197;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 807; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 391 AAAGGTGAGAAAGAGATTCGGTGAACATAGACCCCTGGTCTTAATGAGAAACAGGC 450  
QY 420 CTCCCATGTGATGACAGCACTGGGCAAGCCATCGGGAGATGAGAACACAGGTCTCT 479  
DB 451 CTCCCATGTGATGACAGCACTGGGCAAGCCATCGGGAGATGAGAACACAGGTCTCT 510  
QY 480 CAGGTGACACGAGCTCAAGTTCTCAAGATGCTGCGCGGTGTCGCGAGACGAG 539  
DB 511 CAGGTGACACGAGCTCAAGTTCTCAAGATGCTGCGCGGTGTCGCGAGACGAG 570  
QY 540 AGCAAGATCTACCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599  
DB 571 AGCAAGATCTACCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630  
QY 600 CAGGGCCCGGGGGGAG 659  
DB 631 CAGGGCCCGGGGGGAG 690  
QY 660 GCATACCTGCGGCAAGCGGCTGGCCCGGTCTTTCATCGGCATCAACGACTGTGAGAG 719  
DB 691 GCATACCTGCGGCAAGCGGCTGGCCCGGTCTTTCATCGGCATCAACGACTGTGAGAG 750  
QY 720 GAGGGCGGCTTGTGTACTCTGACCACTTCCCATGCGGACCTTCAACAGTGGCGAGC 779  
DB 751 GAGGGCGGCTTGTGTACTCTGACCACTTCCCATGCGGACCTTCAACAGTGGCGAGC 810  
QY 780 GGTGAGCCCAACAGCTGAG 839  
DB 811 GGTGAGCCCAACAGCTGAG 870  
QY 840 TGGAAAG 899  
DB 871 TGGAAAG 930  
QY 900 ATGTGAGCTTCAAGCTGAG 959  
DB 931 ATGTGAGCTTCAAGCTGAG 990





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GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 17, 2004, 03:37:49 ; Search time 588 Seconds  
(without alignments)  
2419.376 Million cell updates/sec

Title: US-09-806-277A-6  
Sequence: 1 MRGALVGVILSLAFLSL.....NDVACHTTMTFMCPEFDKEM 271

Perfect score: 1441  
Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=PCT THR MAX=100 -THR MIN=0 -ALIGN=15  
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-USER=US09806277.qcgn.1.1-885@runat.15122004.101627.29241 -NCPU=6 -ICPU=3  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

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3: geneseqn2000s:\*  
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6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
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10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1441	100.0	1238	3	Aa265084 Membrane
3	1441	100.0	1238	3	AaC58385 Human PRO
4	1441	100.0	1238	5	AA44230 Human PRO
5	1441	100.0	1238	6	Ab188155 Human PRO
6	1441	100.0	1238	6	Ab195644 Human ang

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8	1441	100.0	1238	8	ABX80858	ABX80858 Human sec
9	1441	100.0	1238	8	ACD44367	ACD44367 CDNA enco
10	1441	100.0	1238	8	ABX79538	ABX79538 Human sec
11	1441	100.0	1238	8	ACA93559	ACA93559 Novel hum
12	1441	100.0	1238	8	ABX81241	ABX81241 Novel hum
13	1441	100.0	1238	8	ACA93057	ACA93057 Novel hum
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15	1441	100.0	1238	8	ACA67996	ACA67996 Novel hum
16	1441	100.0	1238	9	ACA88445	ACA88445 Human sec
17	1441	100.0	1238	9	ACD81952	ACD81952 CDNA enco
18	1441	100.0	1238	9	ADA37867	ADA37867 Human CDN
19	1441	100.0	1238	9	ADA21553	ADA21553 Human CDN
20	1441	100.0	1238	9	ADA10340	ADA10340 Human CDN
21	1441	100.0	1238	9	ADA17884	ADA17884 CDNA enco
22	1441	100.0	1238	9	ADA27992	ADA27992 Human CDN
23	1441	100.0	1238	9	ADA94572	ADA94572 Human CDN
24	1441	100.0	1238	9	ADA38797	ADA38797 Human CDN
25	1441	100.0	1238	9	ADA92918	ADA92918 Human CDN
26	1441	100.0	1238	9	ACH65513	ACH65513 Human CDN
27	1441	100.0	1238	9	ADA22479	ADA22479 Human CDN
28	1441	100.0	1238	9	ACD39503	ACD39503 Human sec
29	1441	100.0	1238	9	ADA06645	ADA06645 Human sec
30	1441	100.0	1238	9	ADA39338	ADA39338 Human CDN
31	1441	100.0	1238	9	ADB96364	ADB96364 Human PRO
32	1441	100.0	1238	10	ADC57836	ADC57836 Human PRO
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34	1441	100.0	1238	10	ADC12067	ADC12067 Human CDN
35	1441	100.0	1238	10	ADC56489	ADC56489 Human PRO
36	1441	100.0	1238	10	ADC07544	ADC07544 Human CDN
37	1441	100.0	1238	10	ADC11534	ADC11534 Human CDN
38	1441	100.0	1238	10	ADC14656	ADC14656 Novel hum
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## ALIGNMENTS

RESULT 1	ABA91201	standard; DNA; 813 BP.
ID	ABA91201	standard; DNA; 813 BP.
XX	ABA91201	
AC	ABA91201	
XX	19-FEB-2002 (first entry)	
DT	19-FEB-2002	
XX	Human collectin polynucleotide SEQ ID NO 45.	
DE	Human collectin; Cl-L2-1; Cl-L2-2; mouse; antibacterial; virucide;	
XX	Human; collectin; Cl-L2-1; Cl-L2-2; mouse; antibacterial; virucide;	
KW	protein therapy; infection; ds.	
XX	Homo sapiens.	
OS	MO200181401-A1.	
XX	01-NOV-2001.	
PD	23-APR-2001; 2001WO-JP003468.	
XX	21-APR-2000; 2000JP-00120358.	
PR	(FUSO ) FUSO PHARM IND LTD.	
PA	Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y,	
XX	WPI; 2002-055345/07.	
DR	New collectin family proteins, designated Cl-L2-1 and Cl-L2-2, expressed	
XX		
PT		

PT in kidney and for treatment and prevention of bacterial and viral  
infections.

XX Claim 2, Page 121, 134pp, Japanese.

XX The invention relates to human collectin family proteins (CL-L2-1 and CL-  
L2-2, sequences given in the specification, ABB56407-ABB56411 and  
CC ABB56414-ABB56416), their derivatives and fragments and a related  
collectin (CL-L2) of mouse origin (ABB56412) and polynucleotides encoding  
all or part of the proteins. The proteins have antibacterial and virucide  
activity and are used for protein therapy and treatment, prevention and  
diagnosis of bacterial and viral infections. The present sequence is that  
of a collectin polynucleotide of the invention.

XX Sequence 813 BP; 183 A; 225 C; 271 G; 134 T; 0 U; 0 Other;

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Pred. No.:	2,04e-90	Length:	813
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Best Local Similarity:	100.00%	Mismatches:	0
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US-09-806-277A-6 (1-271) x ABA91201 (1-813)

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DB 181 GTCCGGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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QY 101 GlyProProGlyIyProAlaGlyIyProGlyIyLeuProCysGlyIyCysSerGlnLeuIlyg 120
DB 301 GGAACCCCTGGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 121 AlaIleGlyIyGluMetCAspAspGlnValSerGlnLeuThrSerGlnLeuIlyspheIleIys 140
DB 361 GCCATCGGGAGATGAGCAACAGAGTCTTCAGCTGACAGAGAGAGAGAGAGAGAGAGAG 420
QY 141 AsnAlaValAlaGlyValaIyGluIyThrGlySerIlyIleIyLeuLeuValIlysgIyGlu 160
DB 421 AATGCTGTCCCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 161 LysArgIyTrpAlaAspAlaGlnLeuSerCysGlnIlyIyArgIyGlyIyThrLeuSerMetPro 180
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QY 181 LysAspGlnAlaAlaAspGlyLeuMetAlaAlaIyTrpLeuAlaGlnAlaIyLeuAlaArg 200
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DB 601 GTCTTCATCGGAGATCAACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 221 ProMetArgIyThrPheAsnIlyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 240
DB 661 CCATGCGGAGCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
```

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QY 241 AspCysValaIyMetValaIaSerGlyIyIyTrpAsnAspValaIaCysHisIyThrMet 260
DB 721 GACTGCGTGAAGATGGGGCTCGGGGCGCTGGAACGACGCTGCGCACACACCATG 780
QY 261 TyrPheMetCysGlnPheAspIlysgIyAsnMet 271
DB 781 TACTTCATGTGTAGATTGTGACAGAGAGACATG 813
RESULT 2
AAZ5084
AAZ5084 standard; cDNA; 1238 BP.
AC AAZ65084;
AC 05-APR-2000 (first entry)
DT 05-APR-2000 (first entry)
DE Membrane-bound protein PRO1182 encoding cDNA.
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX Homo sapiens.
XX OS
XX PN WO963088-A2.
PD 09-DEC-1999.
XX
XX PF 02-JUN-1999; 99WO-US012252.
XX
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 05-JUN-1998; 98US-0088367P.
XX 05-JUN-1998; 98US-0088202P.
XX 05-JUN-1998; 98US-0088212P.
XX 05-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.
XX 10-JUN-1998; 98US-0088722P.
XX 10-JUN-1998; 98US-0088730P.
XX 10-JUN-1998; 98US-0088734P.
XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088740P.
XX 10-JUN-1998; 98US-0088741P.
XX 10-JUN-1998; 98US-0088742P.
XX 10-JUN-1998; 98US-0088810P.
XX 10-JUN-1998; 98US-0088811P.
XX 10-JUN-1998; 98US-0088824P.
XX 10-JUN-1998; 98US-0088825P.
XX 10-JUN-1998; 98US-0088826P.
XX 11-JUN-1998; 98US-0088858P.
XX 11-JUN-1998; 98US-0088861P.
XX 11-JUN-1998; 98US-0088863P.
XX 11-JUN-1998; 98US-0088876P.
XX 12-JUN-1998; 98US-0088909P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089440P.
XX 16-JUN-1998; 98US-0089512P.
XX 16-JUN-1998; 98US-0089514P.
XX 17-JUN-1998; 98US-0089532P.
XX 17-JUN-1998; 98US-0089538P.
XX 17-JUN-1998; 98US-0089598P.
XX 17-JUN-1998; 98US-0089599P.
XX 17-JUN-1998; 98US-0089600P.
XX 17-JUN-1998; 98US-0089653P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 18-JUN-1998; 98US-0089909P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090423P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090547P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0090865P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 12-AUG-1998; 98US-0096375P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.

PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096953P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097977P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chan J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood W, Yuan J;
PI WPI; 2000-072883/06.
DR P-PSDB; AAY66738.
XX
XX Membrane-bound proteins and related nucleotide sequences.
PT
XX Claim 2; Fig 251; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,11e-90 Length: 1238
Score: 1441.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x AA265084 (1-1238)
QY 1 MetAArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuIleu 20
DB 67 ATGAGGGGGAAATCTGGCGCTGTGGCGCTTAAATCAAGCCCTGGCGCTTCTGACTGCTG 126
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
DB 127 CCATCTGGACATCTCTCAAGCCGCGCGATACCGCTGCTGTGCAAGATCTGTCCT 186
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaPProGlyAysPProGlyAys 60
DB 187 GGCCTCAAGGGGATGCGGGAGAGAGAGCAAAAGCGCCCGCGCGCTGGAGAGA 246
QY 61 ValGlyProThrArgLysGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80
```



Db 307 CGTATGAAAAATTGTCCTCCATTCGCTTAAGGTGAGAAAGAGATTCCGGTGACATA 366  
Qy 101 G1yProPog1yProAeng1yGluProG1yLeuProCysG1ySerG1nLeuArg1yS 120  
Db 367 GGACCCCTGCTGCTCAATGAGAACCAAGCCCTCCATGTGATGACGACCATGGCAAG 426  
Qy 121 A1a1leg1yG1uMeAaspAeng1yValSerG1nLeuThrSerG1uLeu1yPhe1le1yS 140  
Db 427 GCCATCGGGAGATGACCAACAGGTCTCTCACTGACGACGAGCTCAAGTTCATCAAG 486  
Qy 141 Aen1a1Val1a1ag1yValArg1uThrG1uSer1y1e1yTrLeuLeuVal1yG1uG1u 160  
Db 487 AATGCTGCGCGGTGCTCGCGAGACGAGACCAAGATCTACCTGCTGTGTAAGAGAG 546  
Qy 161 LybArg1yTr1a1aPAlaG1nLeuSerCysG1nG1yArg1yG1yTh1e1uSerMetPro 180  
Db 547 AAGCGCTCGCGGAGCGCCAGCTGCTCGCCAGGCGCCGCGGAGCAGCTGAGCATGCC 606  
Qy 181 LybAaspG1uA1a1aAeng1yLeuMeA1a1aTr1e1uA1a1aG1yLeuA1a1aArg 200  
Db 607 AAGAGCGAGGCTGCAATGCTGTATGCGCCGATCTCGGCGCAAGCCGCGCTGCGCGT 666  
Qy 201 ValPhe1leg1y1e1aenAaspLeuG1u1yG1uG1yA1aPheVal1ySerAasp1ySer 220  
Db 667 GCTTCATCGGCATCAACGACCTGAGAGAGGCGCGCTTCGTGTACTGTGACCATCC 726  
Qy 221 ProMeA1yG1hrPheAen1ySTrParSerG1yG1uProAenAen1yTrAaspG1uG1u 240  
Db 727 CCCATGCGGACCTTCACAGAGGCGGAGCGGTGAGCCCAATGCTTACGACGAGAG 786  
Qy 241 AapCysVal1yG1uMeVal1a1aSerG1yG1yTrPheAenAen1yA1aCysH1eTh1eMet 260  
Db 787 GACTGCGAGATGATGCTCGGCGGCTGAGAACGAGCTGCGCTGCAACCAACCATG 846  
Qy 261 TyrPheMeCysG1uPheAasp1ySerG1uAenMet 271  
Db 847 TACTTCATGTGTGATTGACAGAGAAACATG 879

RESULT 4  
AAFA4230  
ID AAFA4230 standard; cDNA, 1238 BP.  
XX  
AC AAFA4230;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO1182 (UNQ596) nucleotide sequence SEQ ID NO:356.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytostratic; cell death;  
KW cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US008439.  
XX  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 98US-014037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US000365.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Garbar H, Gertlisen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kijavlin ID, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WJ,  
PI Zhang Z;  
XX  
XX WPI; 2001-032160/04.  
XX  
XX P-PSDB; AAB65261.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target bioactive  
PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
PT to cause targeted cell death.  
XX  
XX Claim 2; Fig 251; 935pp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
CC be used for targeted delivery of bioactive molecules, such as toxins,  
CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
CC DNA. They may also be used to produce transgenic animals which are used  
CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
CC and protein sequence can be used for tissue typing and in treating  
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAFA4270 to  
CC AAFA4470 represent PCR primers and hybridisation probes used in the  
CC isolation of human PRO sequences. AAFA4087 to AAFA4269 and AAB5154 to  
CC AAB65300 represent human PRO polynucleotide and protein sequences given  
CC in the exemplification of the present invention  
XX  
XX SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 3,11e-90 Length: 1238  
XX Score: 1441.00 Matches: 271  
XX Percent Similarity: 100.00% Conservatave: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 5 Gaps: 0  
XX  
XX US-09-806-277A-6 (1-271) x AAFA4230 (1-1238)  
Qy 1 MetArgG1yAen1e1uA1a1e1uA1yVal1e1u1e1Ser1e1uA1a1e1e1uSer1e1u 20  
Db 67 ATGAGGGGGAAATCTGCGCTGTGTGGCTTCTATTCAGCCGCTTCCTGTCTCATCTG 126  
Qy 21 ProSerG1yH1sProG1nProA1a1yA1yAaspA1a1yA1aProG1yArgProG1yArg 40  
Db 127 CCATCTGACATCTCTCAAGCGCGCTGGAGATGACCGCTGTGTGACATCTGTCTCCT 186  
Qy 41 G1yLeu1ySerG1yAaspA1a1yG1yG1yA1yAaspA1a1yA1aProG1yArgProG1yArg 60  
Db 187 GGCTCTCAAGGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
Qy 61 Val1yProThrG1yG1u1yG1yA1yAaspMeC1yA1yA1yG1yG1yG1ySer1yG1y 80  
Db 247 GTCGCGCCCAACGAG 306  
Qy 81 ArgH1aG1ySer1yG1yPro1yG1ySer1yG1yG1yG1yA1yAaspSerG1yA1yA1e 100

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Db 307 CGTCATGAAAANTTGGTCCCATTTGGCTTAAAGGTGAGAAAGAGATTCCGGTGACATA 366
Qy 101 GTPProBProGlyProBaNGlyGluProGlyLeuProCybGluuysSerGluLeuAlylys 120
Db 367 GGAACCCCTGGTCTTAATGAGAACAGAGCCCTCCCATGTAGTGCAGCCAGCTGGCAG 426
Qy 121 AAlaIleGlyLeuMetAaPaNGInValSerGlnLeuThzSerGluLeuUlySpheIleLys 140
Db 427 GCCATCGGGAGATGAGCAACAGAGCTCTCAGGTGACAGAGAGCTCAAGTTCATCAAG 486
Qy 141 AaMaIaValaIaGlyValaGlyThaGlySerLysIleThyLeuVallyGluGlu 160
Db 487 AATGCTGTCCGCGGTGCGGAGACGAGCAAGATCTTCACTGCTGTGAAGAGAGAG 546
Qy 161 LysArgTyrIaAaPaIaGlnLeuSerCybGlnIyValGlyGlyThrLeuSerMetPro 180
Db 547 AAGCGCTACGCGAGCGCCAGCTCTCTGCGAGGCGCGGGGAGCAGCTGAGCATGCC 606
Qy 181 LysAaPaIaValaIaAaNGlyLeuMetAaIaIaTyrLeuAaGlnaIaGlyLeuAaIaArg 200
Db 607 AAGAGCAGAGCTGCGCAATGGCTGATGGCCGATACCTGGCGCAAGCCGCGCTGGCCGT 666
Qy 201 ValPheIleGlyIleAaMaPaLeuGluLysGluIyValaPheValIyTyrSerAaPaHisSer 220
Db 667 GCTTCATCGGATCAACAGACTGAGAGAGAGGAGGCGCTTGTGTACTGTGACACTCC 726
Qy 221 ProMeIaGlyThrPheAaMaIyTyrPArSerGlyGluProAaMaMaIaIaTyrAaPaGlu 240
Db 727 CCCATCGGAGCTTCAACAGTGGCGAGCGCTGAGCCCAACATGCTACGAGAGAGAG 786
Qy 241 AaPaCyValaIaGluMetValaIaSerGlyIyTyrPheAaPaValaIaCybHisThThMet 260
Db 787 GACTGCGTGAAGATGTGTGCTCGGGCGGCTGAGAACGACGTGGCTGCCACACCATG 846
Qy 261 TyrPheMetCybGluPheAaPaIyGluAaMaMet 271
Db 847 TACTTCATGTGTGAGTTGACAAAGAGAACATG 879

RESULT 5
ABL88155
ID ABL88155 standard; cDNA; 1238 BP.
AC ABL88155;
DT 16-MAY-2002 (first entry)
DE Human PRO1182 cDNA sequence SEQ ID NO:167.
KW Human; angiogenesis; cardiact; cyrostatic; antiangiogenic; hypotensive;
vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
gene therapy; cardiovascular disorder; endothelial disorder; cancer;
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
age-related macular degeneration; arterial restenosis; angina;
rheumatoid arthritis; myocardiial infarction; thrombophlebitis;
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
wound healing; chromosome mapping; gene mapping; gene; se.
XX Homo sapiens.
OS
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222655P.
PR 17-AUG-2000; 2000US-00643657.

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PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0249223P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00786498.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00860280.
PR 25-MAY-2001; 2001US-00860334.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.

XX (GETH ) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gertlesen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WT, Ye W;
XX WPI; 2002-090516/12.
XX P-FSDB; ABB84900.
DR One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 2; Fig 167; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB8503. The PRO proteins and polynucleotides have cardiact, cyrostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
XX SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 3,11e-90 Length: 1238
XX Score: 1441.00 Matches: 271
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: Gaps: 0

US-09-806-277A-6 (1-271) x ABL88155 (1-1238)
Qy 1 MetArgIyLeuMetValaIaGlyValaGlyThaGlySerLysIleThyLeuVallyGluGlu 20

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Db 67 ATGAGGGGAATCTGCGCTGGGCGGTTCTATCAGCTGGCTTCTCTGCTGCTG 126  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCATCTGACATCTCCACGCGCTGGCGCATGACGCTGCTGCTGCTGCTGCTGCT 186  
 QY 41 GILYLeuLysGlyAspAlaGlyValLysGlyAspLysGlyValaProGlyAArgProGlyArg 60  
 Db 187 GGCCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
 QY 61 ValGlyProThrGlyGlyLysGlyLysAspMetGlyAspLysGlyLysGlySerValGly 80  
 Db 247 GTCGGCCCAACGCGAG 306  
 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyLysGlyLysGlyLysGlyLys 100  
 Db 307 GGTATGAGAAAATTGGTCCCTGCTTAAAGGTGAGAAAGAGATTCCTCGGTACATA 366  
 QY 101 GLYProProGlyProAsnGlyValLysProGlyLeuProGlyCysSerGlyLeuArgLys 120  
 Db 367 GGAACCCCTGGTCTTATGAGAACCAAGGCTCCCATGTGAGTGAAGCCAGCTGCGCAG 426  
 QY 121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
 Db 427 GCCATCGGGGAGATGACACCAAGGTCCTCTGCTGACGACCAAGGAGCTCAAGTTCATCAAG 486  
 QY 141 AsnAlaValAlaGlyValArgGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 160  
 Db 487 AATGCTGTGCGCGGTGTCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
 QY 161 LysArgGlyTyrAlaAspAlaGlyLysSerCysGlnGlyArgGlyLysGlyLysLeuSerMetPro 180  
 Db 547 AAGCGCTTACGCGAG 606  
 QY 181 LysAspGlnAlaAlaAsnGlyLysMetAlaAlaIleLysAlaGlnAlaGlyLysAlaArg 200  
 Db 607 AAGGACGAGGCTGCCAATGGCTGATGGCCGATCTGCGGCAAGCCGGCTGGCCGCT 666  
 QY 201 ValPheIleGlyIleAsnAspLeuGlyLysGlyLysGlyLysAlaPheValTyrSerAspHisSer 220  
 Db 667 GTCTTCATCGCGCATCAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
 QY 221 PrometArgThrPheAsnLysTyrPheSerGlyGlyLysProAsnAlaTyrAspGlnLys 240  
 Db 727 CCCATGCGGAGCTTCAACAGTGGCGAGCGGTGAGCCCAATGCTTACGACAGGAG 786  
 QY 241 AspCysValGlyMetValAlaSerGlyLysTyrPheAspValAlaCysHisThrThrMet 260  
 Db 787 GACTGCGTGGAGATGCTGGCTCGGGCGGCTGGAGAGAGAGAGAGAGAGAGAGAGAG 846  
 QY 261 TyrPheMetCysGlyLysPheAspLysGlyLysMet 271  
 Db 847 TACTTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879  
 Db 847 TACTTCATGTGTGAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879  
 RESULT 6  
 ABL95644  
 ID ABL95644 standard; cDNA; 1238 BP.  
 AC ABL95644;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related cDNA PRO1182 SEQ ID NO: 167.  
 XX  
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiact; cytoskeletal; angiogenic; hypotensive; vulnerary;  
 KW antiarteriosclerotic; gene; 86.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200208284-A2.  
 XX  
 XX

PD 31-JAN-2002.  
 XX  
 PF 09-JUL-2001; 2001WO-US021735.  
 XX  
 PR 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220646P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 02-AUG-2000; 2000US-0222695P.  
 PR 17-AUG-2000; 2000US-00643657.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 07-SEP-2000; 2000US-0230978P.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006656.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00816744.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854288.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (BAKE ) BAKER K P.  
 PA (PERRR ) PERRARA N.  
 PA (GERB ) GERBER H.  
 PA (GERRR ) GERRITSEN M E.  
 PA (GODD ) GODDARD A.  
 PA (GODO ) GODOWSKI P J.  
 PA (GURN ) GURNEY A L.  
 PA (HILL ) HILLMAN K J.  
 PA (HILL ) HILLMAN K J.  
 PA (MARS ) MARSTERS S A.  
 PA (PANU ) PAN J.  
 PA (PAON ) PAONI N F.  
 PA (STEP ) STEPHAN J F.  
 PA (WADA ) WATANABE C K.  
 PA (WILL ) WILLIAMS P M.  
 PA (WOOD ) WOOD W I.  
 XX  
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
 DR WPI; 2002-171999/22.  
 DR P-PSDB; ABB95506.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX  
 PS Claim 1; Fig 167; 567pp; English.  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

# Alignment Scores:

Score:	3.11e-90	Length:	1238
Percent Similarity:	1441.00	Matches:	271
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-806-277A-6 (1-271) x ABL95644 (1-1238)

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Db 67 ATGAGGGGGAAATCGGCGCTGGTGGGCGCTTAATCAAGCCCTGCTGCTCACTGCTG 126
QY 21 ProSerGlyHisProGlnProAlaGlyAAspAspAlaCySerValGlnIleLeuValPro 40
Db 127 CCATCTGGACATCCTCAGCCGGCTGGCGATGACCGCTGCTGTGCGAGATCCTGCTCCT 186
QY 41 GlyLeuLysGlyAAspAlaGlyGlyLysGlyAAspLysGlyAlaProGlyAAspProGlyAAsp 60
Db 187 GAGCTCAAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 61 ValGlyProThrGlyGlyLysGlyAAspMetGlyAAspLysGlyGlyLysGlySerValGly 80
Db 247 GTGGGCGCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAAspSerGlyAAspIle 100
Db 307 CGTATGGAGAAATTTGGTCCATTCCTTAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
QY 101 GlyProProGlyProAAspGlyGlyLysProGlyLysProGlyLysProGlyLysProGlyLys 120
Db 367 GAGACCCCTGCTGCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
QY 121 AlaIleGlyLysMetAAspAspGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140
Db 427 GCCATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
QY 141 AsnAlaValAlaGlyValArgGlyLysThrGlyLysSerLysIleTyrLeuLeuValLysGly 160
Db 487 AATGCTGCGCGGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
QY 161 LysArgTyrAlaAAspAlaGlnLeuSerCySerGlnGlyArgGlyGlyTyrLeuSerMetPro 180
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QY 201 ValPheIleGlyIleAAspLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 220
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RESULT 7
AC64399
ID AC64399 standard; cDNA; 1238 BP.
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AC AC64399;
XX
DT 17-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1182 cDNA.
XX
KW Human; secreted and transmembrane protein; cytosolic; anti-HIV;
KW vrinolide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.
XX
OS Homo sapiens.
XX
PN US200300531-A1.
XX
PD 02-JAN-2003.
XX
PF 19-NOV-2001; 2001US-0089734.
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PR 16-JUN-1997; 97US-0049787P.
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PR 17-JUN-1998; 98US-0089653P.

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PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004341.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 10-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006319.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US023031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023528.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
PA (GENTH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Garber H, Gerltzen ME, Goddard A, Godowski PJ,  
PI Gilmaldi JC, Gunney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z,  
XX  
XX WPI, 2003-352829/33.  
DR P-PSDB; AB072552.  
XX  
XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
PT disease.  
XX  
XX Claim 1, Fig 251, 663pp; English.  
XX  
XX The invention describes a new isolated nucleic acid molecule comprising  
CC the full length coding sequence of the DNA deposited with the American  
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PA, 819-PA,  
CC 209439, 20133, etc.) or a sequence with at least 80% identity to a DNA  
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
CC are particularly useful for detecting or treating e.g. malignancies or  
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,

CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
CC disease in mammals. The PRO polypeptides are useful in drug screening,  
CC particularly as targets for therapeutic intervention in these diseases,  
CC and in the diagnostic determination of the presence of these diseases.  
CC The PRO polypeptides are also useful as molecular weight markers, or for  
CC chromosome identification. The PRO genes are useful as hybridisation  
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
CC The PRO genes may also be used in gene therapy, particularly for  
CC replacing a defective gene. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide  
XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 3,11e-90 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
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DB 67 ATGAGGGGGAATCTGGCCCTGCTGTAACTACAGCCCTGGCCCTTCTCACTGCTG 126  
QY 21 ProSerGlyHisProGlnProAlaGlyAaPaaPaaIaCySerValGlnIleLeuValPro 40  
DB 127 CCACTGTGACATCTCTCAAGCCGGCTGGCGATACCCCTCTCTGTGCAATCTCTCCCT 186  
QY 41 GlyLeuLygIyAaPaaIaGlyGlyIyLygIyAaPlyLygIyAaProGlyAaPProGlyAa 60  
DB 187 GGCCCTCAAGAGGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrGlyGlyIyLygIyAaPmerGlyAaPlyLygIyGlyIyAaPlyLygIy 80  
DB 247 GTGGCCCGGAG 306  
QY 81 ArgHisGlyLybIleGlyProIleGlySerIyLygIyGlyIyAaPserGlyAaPlyIle 100  
DB 307 CGTATGGAAGAAATTTGGTCCATTTGGCTCTAAGGTGAAGAGAGAGAGAGAGAGAGAG 366  
QY 101 GlyProProGlyProAaGlyGlyIyProGlyLeuProGlyGlyGlyGlyGlyGlyGly 120  
DB 367 GGACCCCTGCTCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
QY 121 AlaIleGlyIyGlyIyAaPaaIaGlyIyAaPserGlyIyLeuThrSerGlyIyLeuPheIle 140  
DB 427 GCCATCGGGAG 486  
QY 141 AaPaaIaValaIyAaIyAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIy 160  
DB 487 AATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 161 LybArgIyAaIaPaaIaGlyIyAaPserGlyGlyIyAaGlyIyAaGlyIyAaGlyIy 180  
DB 547 AAGGCTAAGCGGAG 606  
QY 181 LybAaPaaIaIaIaAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIy 200  
DB 607 AAGGAG 666  
QY 201 ValPheIleGlyIyIaAaPaaIaGlyIyAaPserGlyIyAaPheValIySerAaPaaI 220  
DB 667 GTCTTCATCGGATCAACAG 726  
QY 221 ProMetAaGlyThrPheAaPlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIy 240  
DB 727 CCATGCGAG 786  
QY 241 AaPaaIaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIyAaGlyIy 260

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Db 847 TACTTCATGTGTGAGTTTGACAGGACAAACATG 879  
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XX  
XX 22-APR-2003 (first entry)  
XX  
DE Human secreted/cranmembrane protein cDNA, #144.  
XX  
KM Human; gene; 88; PRO; secreted; transmembrane; pharmaceutical;  
KM diagnostic; biosensor; bioeactor; tumour; therapeutic; gene therapy;  
KM tumour-associated antigenic target; TAT; ADPPT;  
KM antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
FM US2003027162-A1.  
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XX  
XX 15-NOV-2001; 2001US-00997428.  
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PR 24-NOV-1997; 97US-0066770P.  
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PR 28-APR-1998; 98US-0083322P.  
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PR 04-JUN-1998; 98US-0088030P.  
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PR 16-JUN-1998; 98US-0089512P.  
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PR 07-OCT-1998; 98US-0092114P.
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PR 05-JAN-1999; 99US-0000010P.
PR 08-MAR-1999; 99US-0000502P.
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PR 11-FEB-2000; 2000US-0003565P.
PR 18-FEB-2000; 2000US-0004341P.

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PR 09-JUL-2001; 2001US-0021735P.
PR 28-AUG-2001; 2001US-00941992P.
XX (GENTH) GENENTECH INC.
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerstein ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2003-340824/32.
DR P-PSDB; ABO25998.
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX Claim 2; Fig 251; 661pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/patseq/ident.html
XX SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3,11e-90 Length: 1238
Score: 1441.00 Matches: 271
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-806-277A-6 (1-271) x ACD44367 (1-1238)

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QY 21 ProSerGIYHISProGlnProAlaGlyAspAspAlaCYSerValGlnIleLeuValPro 40  
Db 127 CCATCTGGACATCTCCACCGCGCTGGCCGATGACGCTCTGCTGTCACATCTGCTCCCT 186  
QY 41 GlyLeuLYSGIYAAspAlaGlyGlyLeuLYSGIYAAspLYSGIYAlaIleProGlyIARProGlyIARg 60  
Db 187 GGCCTCAAGGGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCGGAGCGGCTGGAAGA 246  
QY 61 ValGlyProThrGlyGlyLeuLYSGIYAAspMetGlyYAAspLYSGIYAlaIleGlySerAlaGly 80  
Db 247 GTCCGCCCCACGGGAGAAAAGAGACATGGGGGCAAGAAGACAAAGGACAGTGTGGT 306  
QY 81 ArgHISGlyLYSILEGlyProIleGlySerLYSGIYLYSGIYAAspSerGlyYAAspIle 100  
Db 307 CGTCAATGAAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCGGTGACATA 366  
QY 101 GlyProProGlyIProAsnGlyGlyLeuProGlyLeuProCYSerGlyCYSerGlnLeuArgLYS 120  
Db 367 GGACCCCTGGTCTTAATGAGAACCAAGGCTCCCATGTGAGTGCAGCCGCTGGCAAG 426  
QY 121 AlaIleGlyGlyLeuMetAspAsnGlnValSerGlnLeuThrSerGlyLeuLeuPheIleLYS 140  
Db 427 GCCATCGGGAGATGGACACCAAGGTCTCTCAGCTGACAGGACCTCAAGTTCATCAAG 486  
QY 141 AsnAlaValAlaGlyValIARGLuThrGlySerLYSILETYrLeuLeuValIleGlyGlyLeu 160  
Db 487 AATGCTGTCGCGGTGTCGCGAGCGAGACCAAGATCTTACTCTGCTGTAAGAGAGAG 546  
QY 161 LysArgTYrAlaAspAlaGlnLeuSerCYSerGlnIYARgLYSILETYrLeuSerMetPro 180  
Db 547 AAGCGCTACGGGAGCGCCAGCTGCTGCCAGGGCCCGGGGCAAGCTGAGCATGCC 606  
QY 181 LysAspGlyAlaAlaAsnGlyLeuMetAlaAlaTYrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGACGAGGGCTGCAATGGCTGTATGGCCGATACCTGGGCGAGCCGGCTGGCCCGT 666  
QY 201 ValPheIleGlyLYSAsnAspLeuGlyLYSGIYAlaPheValTYrSerAspHisSer 220  
Db 667 GTCTTCACTGGCATCAAGCACTGAGAGAGAGGCGCCTTCTGCTACTGACCACTCC 726  
QY 221 ProMetArgIHPheAsnLYSTyrArgSerGlyGlyProAsnAsnAlaTYrAspGlyLeu 240  
Db 727 CCATGCGGACCTTCACACAGTGGCGGAGCGGTAGCCCAACCAATGCTTACGACAGAGAG 786  
QY 241 AspCysValAlaMetValAlaSerGlyGlyTYrPheAspValAlaCysHisThrThrMet 260  
Db 787 GACTGCGGAGATGTGGCTCGGGCGGCTGGAAAGAGCTGGCTGCACACCACTG 846  
QY 261 TYrPheMetCYSGLuPheAspLYSGIYLeuMet 271  
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RESULT 10  
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ID ABX79538 standard, cDNA, 1238 BP.  
XX  
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AC  
XX 17-APR-2003 (first entry)  
DT  
XX  
XX Human secreted/transmembrane protein cDNA, #144.  
DE  
XX  
XX Human, gene; ss, PRO, secreted, transmembrane, signal peptide;  
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
XX  
XX Homo sapiens.  
XX

PN US2002142961-A1.  
XX 03-OCT-2002.  
XX  
XX 19-NOV-2001; 2001US-00989721.  
XX  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WO-US020069.  
XX 13-NOV-1997; 97US-0065186P.  
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XX 17-SEP-1998; 98WO-US019437.  
XX 07-OCT-1998; 98WO-US021141.  
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XX 05-JAN-1999; 99WO-US000106.  
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XX 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.  
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 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 PA (GETH ) GENENTECH INC.  
 PI Aehkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kijavitt TJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z,  
 XX WPI: 2003-155950/15.  
 DR P-PSDB; ABUS9007.  
 XX  
 PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
 XX  
 PS Claim 2; Fig 251; 647pp; English.  
 XX  
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
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 Pred. No.: 3, 11e-90 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0  
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 QY 21 ProSerGlyValIleProGlnProAlaGlyIleAspAspAlaCysSerValGlnIleValPro 40  
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 QY 41 GlyLeuIleGlyIleAspAlaGlyIleGlyIleValAspIleValAlaProGlyIleArg 60  
 Db 187 GGCCCTCAAGAGGATCGGGAG 246  
 QY 61 ValGlyProThrGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 80  
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 Db 307 CGTCATGGAAAAAATTGGTCCATTGGCTCTAAAGGTGAGAGAGAGAGAGAGAGAGAG 366  
 QY 101 GlyProProGlyIleProAsnGlyIleProGlyIleProGlyIleProGlyIleProGlyIle 120  
 Db 367 GGAGCCCTGGCTGCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
 QY 121 AlaIleGlyIleValMetAspAsnGlnValIleSerGlnLeuThrSerGlnLeuValIle 140  
 Db 427 GCATCGGGAGATGAGACCAACGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486  
 QY 141 AsnAlaValAlaGlyIleValIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 160  
 Db 487 AATGCTGTGCGCCGTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
 QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyIleGlyIleGlyIleGlyIleGlyIle 180  
 Db 547 AAGCGCTACCGGAG 606  
 QY 181 LysAspGlnAlaAlaAsnGlyIleMetAlaIleTyrLeuAlaGlnIleGlyIleValArg 200  
 Db 607 AAGACGAGGCTCCATGAGCTGATGCGCGCATCTGAGCGAGAGAGAGAGAGAGAGAG 666  
 QY 201 ValPheIleGlyIleAsnAspLeuGlyIleGlyIleValAlaPheValIleSerAspHisSer 220  
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 QY 221 ProMetArgThrPheAsnIleTyrPArgSerGlyIleProAsnAsnAlaTyrAspGlnGlu 240  
 Db 727 CCATCGGAGACCTTCAACAGAGTGGCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 786  
 QY 241 AspCysValGlnMetValAlaSerGlyIleTyrAsnAspValAlaCysHisThrMet 260  
 Db 787 GACTGTGAGTGAATGTGTGGCTGCGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 846  
 QY 261 TyrPheMetCysGlnPheAspIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 280  
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 ID ACA93559 standard; cDNA; 1238 BP.  
 AC ACA93559;  
 XX  
 DT 16-JUL-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO1182 cDNA.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185;  
 KW PRO943; PRO1183; PRO1387; PRO5723; PRO1141; PRO3301;  
 KW PRO9940; PRO1181; PRO1170; PRO361; PRO846; bioactive molecule; toxin;



KW radiolabel; antibody; cell death; tissue typing; gene therapy;  
KW cytostatic; chromosome mapping; gene mapping; transgenic animal;  
KW knockout animal; immunohistochemical staining; gene; ss.  
XX Homo sapiens.  
OS  
PN US2003022187-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 14-NOV-2001; 2001US-00993667.  
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PR 17-SEP-1998; 98US-0100858P.  
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 PR 20-FEB-1999; 99WO-US030911.  
 PR 08-MAR-1999; 99WO-US005028.  
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 PR 23-JUN-1999; 99WO-US012252.  
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 PR 30-NOV-1999; 99WO-US028313.  
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 PR 06-JAN-2000; 2000WO-US000219.  
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 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-JUN-2000; 2000US-0213637P.  
 PR 28-JUL-2000; 2000WO-US020710.  
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## Alignment Scores:

Pred. No.: 3, 11e-90  
 Score: 1441.00  
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 DB: 8  
 Gaps: 0

US-09-806-277a-6 (1-271) x ACA93559 (1-1238)

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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 DB 127 CCATCTGGACATCTCCAGCGGCTGCGATGACGCTGCTGTGCAATCTGCTCCCT 186  
 QY 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
 DB 187 GGGCTCAAGGGGATGCGGAG 246  
 QY 61 ValGlyProThrGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 80  
 DB 247 GTGCGGCGCCAGCGGAG 306  
 QY 81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
 DB 307 CGTCATGAGAAATTTGGCTCCCATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366

QY 101 GlyProProGlyProAsnGlyGlyValProGlyLeuProCysSerGlnLeuValArgLys 120  
 DB 367 GGACCCCTGCTCTTAATGAGAGACCAAGCCTCCCATGTGATGAGACAGCTGCGCAAG 426  
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 DB 427 GCCATCGGGAGATGAGACACCAAGCTCTCAGCTGAGCAAGAGAGCTCAAGTTATCAAG 486  
 QY 141 AsnAlaValAlaGlyValArgGlyValThrGlySerLysIleTyrLeuLeuValGlyGlyVal 160  
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 QY 181 LysAspGlyValAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyValArg 200  
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 QY 201 ValPheIleGlyTyrLeuAsnLeuGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 220  
 DB 667 GTCTTCATGCGCATCAACAGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
 QY 221 ProMetArgThrPheAsnLysTyrPargSerGlyValProAsnAsnAlaTyrAspGlyVal 240  
 DB 727 CCATCGGACCTTCAACAGAGTGGCGGAGGCTGAGCCCAACAGGCTCAACAGAGAGAG 786  
 QY 241 AspCysValGlyMetValAlaSerGlyGlyTyrPheAsnValAlaCysHisThrThrMet 260  
 DB 787 GACTGCTGAGAGATGATGCTGCGGCGGCTGGAACGAGTGGCTGCCACACCAACATG 846  
 QY 261 TyrPheMetCysGlyPheAspLysGlyAsnMet 271  
 DB 847 TACTCATGTGATGATTGACAAAGAGACATG 879

## RESULT 12

ABX81241

ABX81241 standard; DNA; 1238 BP.

AC ABX81241;

DT 22-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO1155 DNA.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; db.

OS Homo sapiens.

PN US2003027985-A1.

PD 06-FEB-2003.

PF 14-NOV-2001; 2001US-00990562.

PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-0065186P.  
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 PR 24-NOV-1997; 97US-0066770P.  
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PR 20-MAR-1998; 98US-0078910P.  
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### Alignment Scores:

Pred. No.:	3, 11e-90	1238
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	Length:	1238

US-09-806-277A-6 (1-271) X ABX81241 (1-1238)

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QY	ProSerGIYHIAProGlnProAlaGIYAAPAPAPAlaCYSSerValGlnIleLeuValPro	40
Db	CCATCTGGACATCTCAAGCCGGCTGGTCGATGACGCTCTGCTGTGCAGATCTGTGCTCT	186
QY	GIYLeuLeuGIYAAPAlaGIYGIYGIYGIYGIYAAPLYGIYAlaProGIYArGIYArGIY	60
Db	GGCCTCAAGGGGATCGGGAGAGAGAGAGAGCAAGGCGCCCGGACGCGCTTGGAGA	246
QY	ValGIYProThrGIYGIYLeuYGIYAAPMeGIYAAPLYGIYGIYGIYGIYSerValGIY	80
Db	GTGGGCCCCACGGGAGAAAAGAGACATGGGGGCAAAAGCAGAAAAGCAGATGGGGT	306
QY	ArgHIEGIYLeuIleGIYProIleGIYSerLeuYGIYGIYGIYGIYAAPSerGIYAAPIle	100
Db	CGTCAATGAGAAATTTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCGGGTGACATA	366
QY	GIYProProGIYProAangIYGIYGIYGIYProCYGIYGIYSerGlnLeuAlaArgLYs	120
Db	GGACCCCTGTGCTCAATAGAGAACCAAGGCGCTCCCATGTGATGACGACCACTCGCAAG	426
QY	AlaIleGIYGIYMeLeuAangIYValIleSerGlnLeuThrSerGlnLeuLYsPheIleLYs	140
Db	GGCATCGGGAGATGACACCAAGGCTTCAAGCTTCAAGCGAGAGCTCAAGTTATCAAG	486
QY	AsnAlaValAlaGIYAlaArgGIYThrGIYSerLYsIleTYrLeuLeuValIleGIYGIY	160
Db	AATGCTGTGGCGGCTGTGGCGAGACGAGACAAAGATCACTGCTGTGAAGAGAGAG	546
QY	LYsArgTYrAlaAPAlaGIYLeuSerCYGIYGIYGIYGIYGIYThrLeuSerMePro	180
Db	AACCGCTACCGGGACCGCCAGCTGTCTCGACAGGCGCGGGGGGACCCCTAGCATGCC	606
QY	LYsAAPGIYAlaIleAangIYLeuMeAlaIleTYrLeuAlaGlnAlaGIYLeuAlaArg	200
Db	AAGGACGAGGCTCCCATAGGCTGATGGCGGATACCTGGGCAAGCGCGCTTGGCCGT	666
QY	ValPheIleGIYIleAsnAPLeuGIYLYsGIYGIYAlaPheValTYrSerAPHisSer	220

Dc		667	GCTTCATCGGCATCAACGACTGTGGAGAGAGGCCCTTCGTACTGTACCCTCC	726		
Qy		221	PromoterArgThrPheAsnLysIleTyrArgSerGlyValLeuProAsnAsnAlaTyrAspGlu	240		
Dd		727	CCCATGCGGACCTTAACAAGAATGGGCGCAGCGGTAAAGCCCAACATGCTTAGAGAGAG	786		
Qy		241	AspCysValIGlutMetValAlaSerGlyGlyTyrAsnAspValAlaCysHisIsthThrMet	260		
Dd		787	GACTGGTGTTGAATATGGTGGCCCTCGGGCGCGCTGGAAACGACGTGGCTGCCAACACCATG	846		
Qy		261	TyrPheMetCysGluPheAspLysGluAsnMet	271		
Dd		847	TACTTCATGTGTGAATTGACAAAGAGAAACATG	879		
<b>RESULT 13</b>						
ACAA93057						
ID	ACAA93057	standard; cDNA; 1238 BP.				
XX	AC	ACAA93057;				
XX	DT	16-JUL-2003 (first entry)				
DE	Novel human secreted and transmembrane protein PRO182 cDNA.					
KM	Human; secreted and transmembrane protein; PRO, nocotropic;					
KW	neuroprotective; antiparkinsonian; cytosolic; gene therapy;					
KM	chromosome mapping; gene mapping; transgenic animal; knock-out animal;					
KX	neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;					
XX	gene; ss.					
OS	Homo sapiens.					
PN	US2003017476-A1.					
XX	PD	23-JAN-2003.				
PE	20-NOV-2001,	2001US-00989724.				
XX	PR	16-JUN-1997;	97US-0049787P.			
XX	PR	17-OCT-1997;	97US-0062250P.			
XX	PR	05-NOV-1997;	97WO-US020069.			
XX	PR	12-NOV-1997;	97US-0065186P.			
XX	PR	13-NOV-1997;	97US-0065311P.			
XX	PR	24-NOV-1997;	97US-0066770P.			
XX	PR	25-FEB-1998;	98US-0075945P.			
XX	PR	20-MAR-1998;	98US-0078910P.			
XX	PR	28-APR-1998;	98US-0083322P.			
XX	PR	07-MAY-1998;	98US-0084600P.			
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XX	PR	02-JUN-1998;	98US-0087607P.			
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XX	PR	04-JUN-1998;	98US-0088021P.			
XX	PR	04-JUN-1998;	98US-0088025P.			
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XX	PR	05-JUN-1998;	98US-0088167P.			
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XX	PR	09-JUN-1998;	98US-0088655P.			
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PR 11-JUN-1998; 98US-0088861P.  
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PR 12-JUN-1998; 98US-0088105P.  
PR 16-JUN-1998; 98US-0089440P.  
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PR 01-JUL-1998; 98US-0091360P.  
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PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
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PR 10-AUG-1998; 98US-0095916P.  
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PR 10-AUG-1998; 98US-0096013P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
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PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.

PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
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PR 18-AUG-1998; 98US-0096950P.  
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PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
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PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 31-AUG-1998; 98US-0098052P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113286P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0133957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004431.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-JUN-2000; 2000US-0213637P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.

Alignment Scores: 3.11e-90  
Pred. No.:

Length:

1238

Score: 1441.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 8  
Matches: 271  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-806-277a-6 (1-271) x ACA93057 (1-1238)

QY 1 MetarglyAenleuA1aleuValGlyValIleuIleSerleuA1aPhleuSerleu 20  
Db ATGAGGGGAGATCTGGCCCTGGTGGCTTCTAATCAAGCTTGGCTTCTGCTGCT 126  
QY 21 ProSerGlyHISProGlyInProAlaGlyAAspAAspA1aCysSerValGlnIleleuValPro 40  
Db CCATCTGGACATCTCTCAAGCCGCTGGCATGACCGCTGCTTGTGACAGATCTGTCCT 186  
QY 41 G1YleuYsgGlyAAspA1aGlyGlyIleuYsgGlyAAspGlyA1aProGlyAAspGlyAArg 60  
Db GGCTTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrGlyGlyIleuYsgGlyAAspMetGlyAAspGlyGlyIleuYsgGlySerValGly 80  
Db GTCCGGCCCAAGGAG 306  
QY 81 ArgHISGlyIleuIleGlyProIleGlySerIleuYsgGlyIleuYsgGlyAAspSerGlyAAspIle 100  
Db CGTATGAG 366  
QY 101 G1YProProGlyProAAspGlyGlyIleuProGlyIleuProGlyIleuProGlyIleuAArg 120  
Db GGACCCCTGGTCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
QY 121 A1aIleGlyIleuMetAAspAAspGlyValSerGlyIleuThSerGlyIleuYsgGlyPheIleYs 140  
Db GCCATCGGGGAG 486  
QY 141 AAspA1aValIleuYsgGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleu 160  
Db AATCTGTCGCGGAG 546  
QY 161 LysArgGlyA1aAAspA1aGlnIleuSerCysGlnIleuYsgGlyIleuYsgGlyIleuYsgGlyIleu 180  
Db AAGCGCTACGCGAG 606  
QY 181 LysArgGlyA1aAAspGlyIleuMetA1aA1aIleuYsgGlyIleuYsgGlyIleuYsgGlyIleu 200  
Db AAGAGCGAGGCTGCGCAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666  
QY 201 ValPheIleGlyIleuAAspA1aGlnIleuYsgGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleu 220  
Db GTCTTCATCGGATCAAG 726  
QY 221 ProMetArgThrPheAAspGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleu 240  
Db CCATGCGGAG 786  
QY 241 AspCysValGlyIleuMetValA1aSerGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleu 260  
Db GACTGCGGAG 846  
QY 261 TyrPheMetCysGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleuYsgGlyIleu 271  
Db TACTTCATGCTGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879

XX Human, PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
KM toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
KM protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
antibacterial.  
XX Homo sapiens.  
OS US2002123463-A1.  
XX 05-SEP-2002.  
XX 19-NOV-2001; 2001US-00989732.  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97MO-US020069.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 24-NOV-1997; 97US-006770P.  
XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0078910P.  
XX 28-APR-1998; 98US-0083322P.  
XX 07-MAY-1998; 98US-0084600P.  
XX 28-MAY-1998; 98US-0087106P.  
XX 02-JUN-1998; 98US-0087607P.  
XX 02-JUN-1998; 98US-0087609P.  
XX 02-JUN-1998; 98US-0087759P.  
XX 03-JUN-1998; 98US-0087827P.  
XX 04-JUN-1998; 98US-0088021P.  
XX 04-JUN-1998; 98US-0088025P.  
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XX 04-JUN-1998; 98US-0088028P.  
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XX 04-JUN-1998; 98US-0088326P.  
XX 05-JUN-1998; 98US-0088167P.  
XX 05-JUN-1998; 98US-0088202P.  
XX 05-JUN-1998; 98US-0088212P.  
XX 05-JUN-1998; 98US-0088217P.  
XX 09-JUN-1998; 98US-0088655P.  
XX 10-JUN-1998; 98US-0088734P.  
XX 10-JUN-1998; 98US-0088738P.  
XX 10-JUN-1998; 98US-0088742P.  
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XX 10-JUN-1998; 98US-0088824P.  
XX 10-JUN-1998; 98US-0088826P.  
XX 11-JUN-1998; 98US-0088858P.  
XX 11-JUN-1998; 98US-0088861P.  
XX 11-JUN-1998; 98US-0088876P.  
XX 12-JUN-1998; 98US-0089105P.  
XX 16-JUN-1998; 98US-0089440P.  
XX 16-JUN-1998; 98US-0089512P.  
XX 16-JUN-1998; 98US-0089514P.  
XX 17-JUN-1998; 98US-0089532P.  
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XX 17-JUN-1998; 98US-0089653P.  
XX 18-JUN-1998; 98US-0089801P.  
XX 18-JUN-1998; 98US-0089807P.  
XX 18-JUN-1998; 98US-0089908P.  
XX 16-SEP-1998; 98MO-US019330.  
XX 17-SEP-1998; 98MO-US019437.  
XX 07-OCT-1998; 98MO-US021141.  
XX 01-DEC-1998; 98MO-US025106.  
XX 05-JAN-1999; 99MO-US000106.  
XX 08-MAR-1999; 99MO-US005028.  
XX 02-JUN-1999; 99MO-US012252.  
XX 15-SEP-1999; 99MO-US021090.  
XX 15-SEP-1999; 99MO-US021547.

PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028310.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019592.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ,  
 PI Grijmaldi JC, Gunney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WJ,  
 PI Zhang Z;  
 XX  
 DR WPI; 2003-066810/06.  
 DR P-PsDB; AB010922.  
 PT  
 PT Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers.  
 XX  
 PS Claim 2; Fig 251; 655pp; English.  
 XX

CC The invention relates to a secreted and transmembrane polypeptide, termed  
 CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
 CC useful for detecting PRO polypeptides and for linking a bioactive  
 CC molecule to a cell expressing the above polypeptides, where the bioactive  
 CC molecule is a toxin, radiolabel or an antibody. The bioactive material  
 CC causes the death of the cell. The polypeptide is useful for identifying  
 CC agonists or antagonists of the PRO polypeptide, for preparing variants of  
 CC PRO, as a molecular weight marker for protein electrophoresis purposes  
 CC and the PRO polynucleotide is useful for recombinantly expressing those  
 CC markers. The polynucleotide is also useful as a hybridisation probe, in  
 CC chromosome and gene mapping, in generation of antisense RNA and DNA, in  
 CC the preparation of PRO polypeptide, for generating transgenic animals or  
 CC knockout animals which in turn are useful in the development and  
 CC screening of therapeutically useful reagents, to construct hybridisation  
 CC probes for mapping the gene which encodes PRO and for the genetic  
 CC analysis of individuals with genetic disorders, in gene therapy, for  
 CC chromosome identification, as a chromosome marker and for generating  
 CC probes for PCR, Northern analysis, Southern analysis and Western  
 CC analysis. This sequence represents a human PRO polynucleotide of the  
 CC invention  
 CC

SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,11e-90 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-09-806-277a-6 (1-271) x ABX17141 (1-1238)

QY 1 MetatgglYaenleuAlaleuValGlYalLeuIleSerLeuAlaPheLeuSerLeu 20  
 DB 67 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATACACCTGGCCCTTCTGCATGCTG 126  
 QY 21 ProSerGIYHlSPROGlnProAlaGlYAspAspAlaCysSerValGlnIleLeuValPro 40  
 DB 127 CCAATCTGACATCTCTACACCCGGCTGGCGATACACCTCTCTGTGCAATCTCTCCCT 186  
 QY 41 G1YleuLYsg1YAspAlaGlYglulYsg1YAspLYsg1YAlaProG1YArgProG1YArg 60  
 DB 187 GGCCCTCAAGGGGATGCGGAG 246  
 QY 61 ValG1YProThrG1YglulYsg1YAspMetG1YAspLYsg1YglulYsg1YSerValG1Y 80  
 DB 247 GTCCGCCCCACGGAG 306  
 QY 81 ArgH1sg1YLYs1leG1YProG1leG1YSerLYsg1YglulYsg1YAspSerG1YAsp1le 100  
 DB 307 CGTCATGGAGAAATTTGGTCCCATTTGGCTCTTAAAGGTGAGAGAGAGATTCGGGTACATA 366  
 QY 101 G1YProProG1YProAsnG1YglulYProG1YleuProCYsg1YucYsSerG1nLeuArgLYs 120  
 DB 367 GACCCCTGGTCTTAATGAG 426  
 QY 121 Alal1eg1YglulMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLYsPhe1leLYs 140  
 DB 427 GCCATCGGGAG 486  
 QY 141 AsnAlaValAlaG1YValArgG1uThrg1uSerLYs1leTYrLeuLeuVal1sg1u 160  
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 QY 161 LYsArgTYrAlaAspAlaGlnLeuSerCYsg1nG1YArgG1YTYrLeuSerMetPro 180  
 DB 547 AAGGCTACGGGAG 606  
 QY 181 LYsAspG1uAla1aAsnG1YleuMetAla1aTYrLeuAlaGln1aG1YleuAlaArg 200  
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 QY 201 ValPhe1leG1Y1leAsnAspLeuGlnLYsG1uG1YAlaPheValTYrSerAspH1Ser 220  
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 AC ACA67996;

XX 24-JUN-2003 (first entry)  
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XX Human; secreted and transmembrane protein; gene therapy; PRO; PRO943;  
XX PRO183; PRO184; PRO185; PRO331; PRO1133; PRO363; PRO5723; PRO1387;  
XX PRO1114; PRO3301; PRO9940; PRO1181; PRO1170; PRO361; PRO846;  
XX bioactive molecule; toxin; radiolabel; antibody; cell death; cancer;  
XX autoimmune disease; chromosome mapping; gene mapping; transgenic animal;  
XX knockout animal; septic shock; gene; ss.  
XX Homo sapiens.  
XX OS  
XX US2002177164-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 20-NOV-2001; 2001US-00989293.  
XX  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97MO-US020069.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 24-NOV-1997; 97US-0066770P.  
XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0083322P.  
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XX 02-JUN-1998; 98US-0087609P.  
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XX 18-JUN-1998; 98US-0089907P.  
XX 18-JUN-1998; 98US-0089908P.  
XX 16-SEP-1998; 98MO-US019330.  
XX 17-SEP-1998; 98MO-US019437.  
XX 07-OCT-1998; 98MO-US021141.

PR 01-DEC-1998; 98MO-US025108.  
PR 05-JAN-1999; 99MO-US000106.  
PR 08-MAR-1999; 99MO-US005028.  
PR 02-JUN-1999; 99MO-US012252.  
PR 15-SEP-1999; 99MO-US021090.  
PR 30-NOV-1999; 99MO-US021547.  
PR 01-DEC-1999; 99MO-US028313.  
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PR 20-DEC-1999; 99MO-US030911.  
PR 05-JAN-2000; 2000MO-US000219.  
PR 06-JAN-2000; 2000MO-US000376.  
PR 11-FEB-2000; 2000MO-US003565.  
PR 18-FEB-2000; 2000MO-US004341.  
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PR 15-MAR-2000; 2000MO-US006884.  
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PR 08-NOV-2000; 2000MO-US030952.  
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PR 28-FEB-2001; 2001MO-US006520.  
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PR 20-JUN-2001; 2001MO-US019692.  
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PR 09-JUL-2001; 2001MO-US021735.  
PR 28-AUG-2001; 2001MO-US021922.  
  
XX (GENTH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovere L, Eaton DJ,  
PI Perrera N, Fong S, Gerber H, Gertschen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kijavrin IU, Napier MA, Pan J, Paoi NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX WPI; 2003-328481/31.  
XX P-PDB; AB061674.  
XX  
XX Claim 2; Fig 251; 654pp; English.  
XX  
XX The invention describes an isolated, secreted and transmembrane  
XX polypeptide (I), termed PRO polypeptide. (I) is useful for detecting  
XX PRO943, PRO183, PRO184, PRO185, PRO331, PRO1133, PRO363, PRO5723.  
XX PRO1387, PRO1114, PRO3301, PRO9940, PRO1181, PRO1170, PRO361 or PRO846  
XX polypeptide comprising contacting the sample with the polypeptide and  
XX determining formation of a polypeptide conjugate. (I) is also useful for  
XX linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a  
XX cell expressing the above polypeptides to cause cell death. (I) is also  
XX useful as a therapeutic agent e.g. for treating cancer and autoimmune  
XX disease. PRO is useful in assays to identify other proteins or molecules  
XX involved in binding interactions. The polynucleotide (II) encoding (I) is  
XX useful in chromosome and gene mapping, for generating transgenic animals  
XX or knockout animals which in turn are useful in the development and  
XX screening of therapeutically useful reagents, for the genetic analysis of  
XX individuals with genetic disorders, in gene therapy, for chromosome



CC Identification, and as a chromosome marker. An anti-(I)-antibody is  
CC useful in diagnostic assays for PRO, e.g. detecting its expression in  
CC specific cells, tissues or serum, for affinity purification of PRO, and  
CC for treating septic shock. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide  
XX

SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

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Score:	1441.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
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US-09-806-277a-6 (1-271) x ACA67996 (1-1238)

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Job time : 596 secs

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 06:04:40 ; Search time 101 Seconds

(without alignments)  
1907.166 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 1441

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	317.5	22.0	714	3	US-09-198-603C-26
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4	298.5	20.7	2318	4	US-09-620-312D-733
5	233	16.2	876	4	US-09-535-521-6
6	233	16.2	876	4	US-09-535-521-6
7	233	16.2	2851	4	US-09-535-521-1
8	233	16.2	2851	4	US-09-535-521-3
9	222.5	15.4	1333	3	US-09-227-357-51
10	217.5	15.1	624	4	US-09-535-521-19
11	217.5	15.1	624	4	US-09-535-521-21
12	212.5	14.7	6109	4	US-09-795-061-1

13	212	14.7	6200	4	US-09-795-061-3	Sequence 3, Appli
14	210.5	14.6	6674	4	US-09-620-312D-110	Sequence 110, App
15	210	14.6	6158	4	US-09-918-497-6	Sequence 6, Appli
16	206	14.3	1868	3	US-08-392-367B-1	Sequence 1, Appli
17	206	14.3	1868	3	US-08-893-467A-1	Sequence 1, Appli
18	205.5	14.3	9164	4	US-09-814-915A-80	Sequence 80, Appli
19	204.5	14.2	1323	4	US-09-023-655-013	Sequence 813, App
20	204.5	14.2	1560	3	US-09-453-702B-264	Sequence 264, App
21	204.5	14.2	61663	3	US-09-453-702B-62	Sequence 62, Appli
22	204	14.2	660	4	US-09-169-768-43	Sequence 43, Appli
23	204	14.2	3170	4	US-09-169-768-1	Sequence 1, Appli
24	204	14.2	3171	4	US-09-169-768-15	Sequence 15, Appli
25	204	14.2	3171	4	US-09-169-768-19	Sequence 19, Appli
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44	199	13.8	369	4	US-09-535-521-24	Sequence 24, Appli
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## ALIGNMENTS

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; Patent No. 6787639  
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; APPLICANT: Wakamiya, Noel 6787639ufaka  
; TITLE OF INVENTION: NOVEL COLLECTIN  
; FILE REFERENCE: 19036/36615  
; CURRENT APPLICATION NUMBER: US/09/600, 932  
; CURRENT FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: PCT/JP98/03328  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: JP 10-11281  
; PRIOR FILING DATE: 1998-01-23  
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; SEQ ID NO 1  
; LENGTH: 1595  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
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Cy 1 MetarglyanLeuAlaLeuValGlyValLeuLeuSerLeuAlaPheLeuSerLeuLeu 20



	APPLICANT : MOYER, Shawn S.	
	APPLICANT : RONNING, Michael T.	
	TITLE OF INVENTION : EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC	
	FILE OF INVENTION : YEAST	
	CURRENT APPLICATION NUMBER : A7290	
	CURRENT FILING DATE : US/09/198,603C	
	NUMBER OF SEQ ID NOS : 26	
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Db	360 -AAAAAGTCGGATGTGTATAGTAAGCTTGCTCCAGAAAAGAAAGCTCTGCAACAGA	418
Oy	142 aValAlagLYval-----ArgGlnthrGluSerLYseIl	153
Db	419 AATGGCAAGTATCAAATAAGGCTGACCTTCTCTGGGCAAAACAAGTTGGGAACAAGTT	478
Oy	153 eTYrleuLeuValLYsglulYArgTYrAlasplAglnleuseryGlnGLYAr	173
Db	479 CTTCCTGCAATGTGTAAATATATGACCTTTGAAAAAGTGAAGGCTTGTGTGTCAAGTT	538
Oy	173 gGLYglYThrleuSermetcProLYAspGLUlAlalaENGlyLeumetAlaalATyrle	193
Db	539 CAAGGCTCTGTGGCCACCCCAGGAATAGTCSAAGAAATGAGGCATTCAAGAACTCAT	598
Oy	193 uAlaglnAlagLYleuAlarGValPheIlleGLYlleAsnAspleuglulYBgLYval	213
Db	599 CAAGAG-----GAAGCTTCTGGGCACTCACTGTAGGAAGACAGAAAGGACA	646
Oy	213 aPheValTYrSerAspHiserProMetArg---ThrpheasnLYsrTPArgserGLyl	232
Db	647 GTTTGTG-----GATTCGACAGAAATAGACTGACTTACACAACTGAACAGAGGGTGA	700

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QY      23  UPProAaaAAaAlATyAsrGLUGlUAbSPCyVaIaGluEvaIaIsSrGIyGLTPas 2523
Db       701  ACCCAACAAGCTGGTGTTCGAAGAATTGTGTATTTGCTACTGAAAAATGGCCAGTGAAA 7608
QY      252  naerValaIaCyShieThrThMeTyxPhmeTcySglurhe 266
Db       761  TGAAGTCCCCGTGCACCTCCCAATCGGCCGTCTGTAGTTCC 803

RESULT 4
US-09-620-312D-733
; Sequence 733, Application US/09620312D
; Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Junqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhimei
APPLICANT: John Tillingshaast
APPLICANT: Drmanac, Radote T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_Fl_genes Version 1.0
SEQ ID NO 733
LENGTH: 2318
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (663)..(1691)
US-09-620-312D-733

Alignment Scores:
Pred. NO.:      8,97e-21      Length:      2318
Score:          298.50      Matches:      83
Percent Similarity: 39.67%    Conservative: 38
Best Local Similarity: 27.21%   Mismatches:  119
Query Match:     20.71%        Indels:      65
DB:              4           Gaps:         9

US-09-806-277A-6 (1-271) x US-09-620-312D-733 (1-2318)
QY      21  ProSeRGIyHIEPrOgiInProAlaGlYaBpaPaIaCyBSerValaGlnIlleUenValPro 40
Db       792  CCACCGGCGCCCACGAGGTCCAAGAGGTGACAGAGANTCCACGAGACC-----CCT 842
QY      41  GlYLeuLysGIyaBpaIaGlYGIuLySGIyaBpySGIyAlaPProGIyArgPro----- 58
Db       843  GGCCCAACTGGCAACAAGGACAAGAAAGAGAAAGGGGGGAGCCTGGACCACTGGCCCT 902
QY      59  -----GlyArGVaIGIyProThrgIyGIuLySGIyaBpmetGIyaBpySGIy 74
Db       903  GCGGGTAGAGAGAGCCCATTTGGACACAGCTGGTCCCCCGGAGAGACGTGGCCCAAGCA 962
QY      75  GIuLySGIySerValaGIyArGhiSGIyGIyVilIeGIyProIIeGIySerLySGIyGIuLyB 94

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Db      963 TCTAAAGCTCCAGAGGCCCAAGGCTCCCGTGGTCCCTGGGAAACCCGCGCTCAG 1022
Qy      95  G1YAspSerG1YAsp1Ieg1YProProG1YProAsnG1YIuPProG1YLeuProCyseG1u 114
Db      1023 GGGCCCACTGGGAGACCAAGGCCCCCGGCCCAACAGGAAAGGAACTCCCGGCGCT 1082
Qy      115  -----CySerG1uLeuArg1YAsp1Ieg1YIu----- 124
Db      1083 CAGGCGCCCTCTGCTTCAGAGCACTTCAGGGCACTTGCGGAGCGCTGGGCTGCGA 1142
Qy      124  ----- 124
Db      1143 CCTGGGAGACTGCCAGGCTTCTGGGCTACAGGATGCCAGGCCCAAGGCGCCCCC 1202
Qy      125  -----MetAspAsnG1ValSerG1n 131
Db      1203 GGGCCCTCTGGCCATCAGAGAGCGGTGGTCCCTGGCGCTGCAAGATGAGCCAAACCCG 1262
Qy      132  LeuThrSerG1uLeuYsPhe1IeYAsp1Val1AglYValArgG1uThrG1uSer 151
Db      1263 GCACCGAGAGC-----AATGGCTGCCCGCTCACTGGAAGAACTTCACAGAC 1310
Qy      152  Lys1IeYrLeuLeuVal1YsG1uYsArg1Yr1AAsp1Agl1uLeuSerCyseG1n 171
Db      1311 AAATGCTACTATTTTCTGAGTGAAGAAATTTTGAGATGCAAAAGCTTTCTGTGA 1370
Qy      172  G1YArgG1Yr1LeuSerMetProLYsAsp1u1A1AAsnG1YLeuMet1A1A 191
Db      1371 GACAAGCTTCACACTCTGTTTCATAAACACTAGAGAGAAACGAATGATTAATAA 1430
Qy      192  Tyr1eua1aG1u1AglYLeu1AArgYValPhe1IeG1Y1IeAsnAsp1eG1u1YsG1u 211
Db      1431 CAGATG-----GTAAGGAGAGAGAGCCAGCTGAGTCCCTCAGACACTGAGCGGAA 1484
Qy      212  G1YAlaPheVal1YrSerAsp---HisSerProMetArgThrPheAsnLYrTrpArgSer 230
Db      1485 AACCAATGGAAGTGGCTGATGGACATCTCA-----GACTCAAAAATTTGAAAGCT 1518
Qy      231  G1YIuPProAsnAsn-----AlaTYrAspG1uG1uAspCYsValG1uMetVal 246
Db      1539 GAGACGCGCGATTAACCTGGGCTCATGCGCATGCGCGCAGAGAAAGCTGTGGCTGAT 1598
Qy      247  AlaSerG1Yr1YrAsnAspVal1A1AcyHisThrThrMetYrPheMetCyseG1uPhe 266
Db      1599 TATGCTGGCAGTGGAGATTTCCAAATGTGAAGCTCAATTAATCTTCAATTGCAAAA 1658
Qy      267  AspLYsG1uAsnMet 271
Db      1659 GACAGGGAGACAGTA 1673

```

RESULT 5  
US-09-535-521-4  
Sequence 4, Application US/09535521  
Patent No. 6410714  
GENERAL INFORMATION:

APPLICANT: Weber, Eric R.  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGF RECEPTOR (CANINE CD23)  
FILE REFERENCE: AL-5  
CURRENT APPLICATION NUMBER: US/09/535,521  
CURRENT FILING DATE: 2000-03-24  
EARLIER APPLICATION NUMBER: 60/125,913  
EARLIER FILING DATE: 1999-03-24  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 876  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: CDS

LOCATION: (1)..(876)  
US-09-535-521-4

Alignment Scores:  
Pred. No.: 1,11e-14 Length: 876  
Score: 233.00 Matches: 68  
Percent Similarity: 40.08% Conservative: 37  
Best Local Similarity: 25.95% Mismatches: 110  
Query Match: 16.17% Indels: 47  
DB: 4 Gaps: 6

US-09-806-277a-6 (1-271) x US-09-535-521-4 (1-876)

```

Qy      41  G1YLeuLYsG1YAsp1AglYg1uYsG1YAspLYsG1YAlaPProG1YArgProG1YArg 60
Db      75  GGTGACGTGGCGCTCTGGG---GCTGATGATTCATGCTGTGGCGGCTGCTGAC 131
Qy      61  ValG1YProThrG1Yg1uYsG1YAspMetG1YAspLYsG1Yg1uYsG1YserValG1Y 80
Db      132  CCGTCTCTCTTCTGGCAGAGGACACTGATACAGATCTGAACACAGCTGAGGTCCCGC 191
Qy      81  ArgHisG1YLYs1IeG1YPro1IeG1YserLYsG1Yg1uYs-----G1YAspSer 97
Db      192  CGCCCAAGACGTCTCTCGGGATTCCAAAGACTTGAAGAACACACACAGCTGACAGATGCG 251
Qy      98  G1YAsp1Ie---G1YProProG1YProAsnG1YIuPProG1YLeuPro-CyseG1uCyse 116
Db      252  CCAAGATTCACAGCTGCTCCAGGCTGTCACAGCATGAAAGAAATCCAGCTGAACAGAA 311
Qy      116  rG1uLeuArgLYsAla1IeG1Yg1uMetAspAsnG1Val1SerG1uLeuThrSerG1u 136
Db      312  GAAATGAAGAACCTCAGAGACTGAGCTCCCGAAGCTGAGTCACTTGTGGACT 371
Qy      136  uLYsPhe1IeYsAsn1AVal1AglYValArgG1uThr----- 149
Db      372  GAACAACTCAAGTCCAGAGCTTGAACAGAGAAACACAGCCTTGACTGAGAG 431
Qy      149  ----- 149
Db      432  ACTCCAGAGAGAGCTGAGAGAGCTGTGATGAGCTACAGCTCCAGGCTCCAGATG 491
Qy      150  -----G1uSerLYs1IeYrLeuVal1YsG1 159
Db      492  TAAACGTGCTCCAGAGAGGCTCAACTTCAGAGAGAGTGTACTTCCGCGCAGGA 551
Qy      159  uG1uLYsArgTYr1AAsp1Agl1uLeuSerCyseG1nG1YArgG1Yr1YrLeuSerMe 179
Db      552  GCCCAAGAGTGTATCCAGGCTCGGTTGCTGACCAAGCTGCAAGGGCGCTGGCAG 611
Qy      179  tProLYsAspG1u1A1AAsnG1YLeuMet1A1A1YrLeu1Agl1u1Agl1u1Agl1u1 199
Db      612  CATCCACAGCCCAAGAGAGAGAGAGACTTCTGCGCAGATGCCAACAAGAGGCG----- 666
Qy      199  ArgValPhe1IeG1Y1IeAsnAspLeuG1uYsG1YAlaPheVal1YrSerAsp1 219
Db      667  ---ACCTGATTTGCTCCGAGCTGACAGAGAGGAGGATTTATCTGATGAGCA 722
Qy      219  sSerProMetArgThrPheAsnLYrTrpArgSerG1Yg1uPProAsnAsn1A1YrAsp1 239
Db      723  GAACCCCTG---AACTATGCAACTGCGGCGCGCGGAGCCCAACAACCGGGCCAGGG 779
Qy      239  uG1uAspCYsValG1uMetVal1AAserG1Yr1YrAsnAspVal1A1AcyHisThrTh 259
Db      780  CAGAGACTGCTGATGATGAGAGGCTCGGGCAGTGAATGAGCGCTTCTGGCGCAGCTC 839
Qy      259  rMet 260
Db      840  GCTG 843

```

RESULT 6  
US-09-535-521-6/C  
Sequence 6, Application US/09535521  
Patent No. 6410714

```

GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 876
TYPE: DNA
ORGANISM: Canis familiaris
US-09-535-521-6

Alignment Scores:
Pred. No.: 1,11e-14 Length: 876
Score: 233.00 Matches: 68
Percent Similarity: 40.08% Conservative: 37
Best Local Similarity: 25.95% Mismatches: 110
Query Match: 16.17% Indels: 47
Gaps: 6

US-09-806-277a-6 (1-271) x US-09-535-521-6 (1-876)
QY 41 G1YleuYsg1YAspAlaG1Yg1uYsg1YAspYsg1YAlaPProG1YArgProG1YArg 60
Db 802 GGTGACAGTGGCGCTGCTGGG---GCTGTGATCTGTATCTGTGGGCGGCGCTGTAC 746
QY 61 ValG1YProThrG1Yg1uYsg1YAspMetG1YAspYsg1Yg1uYsg1YserValG1Y 80
Db 745 CCTCTCTCTCTTCTGGACAGGACACTGTACAGAACTGAAACAGCTGAGTGGCGCG 686
QY 81 ArgH1sg1Ys1leG1YPro1leG1Yser1Ysg1Yg1uYs-----G1YAspSer 97
Db 685 CGCCAGAGAGCTCTCTCGGTTTCCAGAGCTTGAAGACACACCGGTGACAGATGGC 626
QY 98 G1YAsp1le---G1YProProG1YProAsnG1Yg1uYProG1YLeuPro-CysG1uYsse 116
Db 625 CCAGAAATCCAGAGCTGCGCTGCTGTCTACAGACATGAGAAATCCAGCTGAACAGAA 566
QY 116 rG1uLeuArg1YsAla1leG1Yg1uMetAspAsnG1NValserG1uLeuThrserG1uLe 136
Db 565 GAGATGAAGACTCAGACTGTGAGCTCTCCAGAACTGGATGACATTGCTGGACT 506
QY 136 uLYsPhe1leLYsAsnAlaValAlaG1YValArgG1uThr----- 149
Db 505 GAACAACCTCAAGTCCAGAGCTTGAACAGAGAAAGACACCTTCATTGACTGAGAG 446
QY 149 ----- 149
Db 445 ACTCCAGAGAGAGTGAAGAAAGCTGTGATGAGACTACAGTGTCCAAAGGCTCCGAGTG 386
QY 150 -----G1uSer1Ys1leY1rLeuLeuValYsg1 159
Db 385 TAACACGTGCGCTGAGAGTGGCTCACTTCCAGAGAAAGTCACTTCCGAGAGGA 326
QY 159 uG1uLYsArg1YrAlaAspAlaG1uLeuSerCysG1uLYsArg1YrLeuSerMe 179
Db 325 GCCCAAGAGTGAATCCAGGCTCGGTTTCTGTGACAGAGCTGCAAGGAGGCGCTGGCCAG 266
QY 179 tProLYsAspG1uAlaAlaAsnG1YLeuMetAla1a1YrLeuAlaG1uLeuAl 199
Db 265 CATCCACAGCCCAAGAGAGAGAGACTTCTGTGCGCAGATATCCCAAGAAAGGCG----- 211
QY 199 ArgValPhe1leG1Y1leAsnAspLeuG1uYsg1YAlaPheValYrSerAspH1 219
Db 210 ----ACCTGGATTGGCTCTCCGGACCTGACAGAGAGGGGAGTTTATCTGATGAGAGA 155
QY 219 sSerProMetArgH1rPheAsnLYsTrpArgSerG1Yg1uProAsnAla1YrAspG1 239
```

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Db 154 GAACCCCTG---AACTATGCAACTGCGCGCGGAGCCCAACACCGGGGCCAGAGG 98
QY 239 uG1uAspCysValG1uMetValAlaAserG1Yg1YrPAsnAspValAlaCysH1srHrTh 259
Db 97 CGAGAGCTGGGTATGATATGACAGGCGCTCGGCGCATGTGAATGACCTTCTGCGCAGCTC 38
QY 259 rMet 260
Db 37 GCTG 34

RESULT 7
US-09-535-521-1
Sequence 1, Application US/09535521
Patent No. 6410714
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2851
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (199)..(1077)
US-09-535-521-1

Alignment Scores:
Pred. No.: 5.76e-14 Length: 2851
Score: 233.00 Matches: 68
Percent Similarity: 40.08% Conservative: 37
Best Local Similarity: 25.95% Mismatches: 110
Query Match: 16.17% Indels: 47
Gaps: 6

US-09-806-277a-6 (1-271) x US-09-535-521-1 (1-2851)
QY 41 G1YleuYsg1YAspAlaG1Yg1uYsg1YAspYsg1YAlaPProG1YArgProG1YArg 60
Db 273 GGTGACAGTGGCGCTGCTGGG---GCTGTGATCTGTATCTGTGGGCGGCGCTGTAC 329
QY 61 ValG1YProThrG1Yg1uYsg1YAspMetG1YAspYsg1Yg1uYsg1YserValG1Y 80
Db 330 CCTCTCTCTTCTGGACAGGACACTGTACAGAACTGAAACAGCTGAGTGGCGCGC 389
QY 81 ArgH1sg1Ys1leG1YPro1leG1Yser1Ysg1Yg1uYs-----G1YAspSer 97
Db 390 CGCCAGAGAGCTCTCTCGGTTTCCAGAGCTTGAAGACACACCGGTGACAGATGGC 449
QY 98 G1YAsp1le---G1YProProG1YProAsnG1Yg1uYProG1YLeuPro-CysG1uYsse 116
Db 450 CCAGAAATCCAGAGCTGCGCTGCTGTCTACAGACATGAGAAATCCAGCTGAACAGAA 509
QY 116 rG1uLeuArg1YsAla1leG1Yg1uMetAspAsnG1NValserG1uLeuThrserG1uLe 136
Db 510 GAGATGAAGACTCAGAGACTGTGAGCTCTCCAGAACTGGATGACATTGCTGGACT 569
QY 136 uLYsPhe1leLYsAsnAlaValAlaG1YValArgG1uThr----- 149
Db 570 GAACAACCTCAAGTCCAGAGCTTGAACAGAGAAAGACAGAGCTTCATTGACTGAGAG 629
QY 149 ----- 149
Db 630 ACTCCAGAGAGAGTGAAGAAAGCTGTGATGAGACTACAGTGTCCAAAGGCTCCGAGTG 689
```

QY 150 -----Glusterlyse11eTyrLeuValLysG1 159  
 Db 690 TAACAGTGGCCGTGAGAGTGGCTCAACTTCAGAGAGAGTCTTACTTCGGCGAGGA 749  
 QY 159 uGluYsArgTyrAlaAspAlaGlnLeuSerCyseGlnGlyArgGlyGlyThrLeuSerMe 179  
 Db 750 GCCCAAGAGTGGATCCAGGCGCGGTTGGCTGCGACAGAGTGCAGAGGCGCGTGGCCAG 809  
 QY 179 tProLYsAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnLysGlyLeuAl 199  
 Db 810 CATCCACAGCAGCAAGAGAGAGAGAGCTTCCTGGCCAGGATGCAACAAGAGGCGC----- 864  
 QY 199 aArgValPheIleGlyIleAsnAspLeuGluLysGlyGlyAlaPheValTyrSerAspH1 219  
 Db 865 ----ACCTGAGATTGGCTCCGCGGACCTGGACAGAGAGGAGGAGTTTATCTGGATGAGCA 920  
 QY 219 sSerProMetArgThrPheAsnLysTyrPArgSerGlyGluProAsnAsnAlaTyrAspG1 239  
 Db 921 GAACCCCTG---AACTATAGCAACTGGCGGCGCGGAGGCCCAACACGGGGCGCAGGG 977  
 QY 239 uGluAspCyseValGlnMetValAlaSerGlyGlyTyrAsnAspValAlaCyseHisThrTh 259  
 Db 978 CGAGGACTGCGTGTATGATGACAGGCGCTCGGGCAGTGAATGACCGCTTCTGGCGAGCTC 1037  
 QY 259 rMet 260  
 Db 1038 GCTG 1041

## RESULT 8

US-09-535-521-3/c  
 ; Sequence 3, Application US/09535521  
 ; Patent No. 6410714  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eric R.  
 ; APPLICANT: McCall, Catherine A.  
 ; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGB RECEPTOR (CANINE CD23)  
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
 ; FILE REFERENCE: AL-5  
 ; CURRENT APPLICATION NUMBER: US/09/535,521  
 ; CURRENT FILING DATE: 2000-03-24  
 ; EARLIER APPLICATION NUMBER: 60/125,913  
 ; EARLIER FILING DATE: 1999-03-24  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2851  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-09-535-521-3

## Alignment Scores:

Score: 5.76e-14 Length: 2851  
 Percent Similarity: 233.00 Matches: 68  
 Best Local Similarity: 40.08% Conservative: 37  
 Query Match: 16.17% Mismatches: 110  
 DB: 4 Indels: 47  
 Gaps: 6

US-09-806-277A-6 (1-271) x US-09-535-521-3 (1-2851)

QY 41 G1YleuYsG1yAspAlaG1yGluYsG1yAspYsG1yAlaProG1yArgProG1yArg 60  
 Db 2579 GGTCAGACTGGCGCTGCTGGG---GCTGGTACTGTATGATGCTGGGCGCGGCTGCTGAC 2523  
 QY 61 ValG1yProThrG1yGluYsG1yAspMetG1yAspYsG1yGlnYsG1ySerValG1y 80  
 Db 2522 CCGTCTCTCTCTTCGGCAGCAGGACACTGTACAAATCTGAAAAGCTGAGTGGCGCCG 2463  
 QY 81 ArgHisG1yYsIleG1yProIleG1ySerIyG1yGluYs-----G1yAspSer 97  
 Db 2462 CGCCCAAGAGCTCTCGGGGTTTCCAGAGACTTGAAAACACACAGGTGACCGATGGC 2403

QY 98 G1YAspIle---G1YProProG1YProAsnG1YgluPProG1YleuPro-CyseG1YCyse 116  
 Db 2402 CCAGAAATCCAGAGCTGGCCAGGTGTACAGAGCATGAGAGAAATCCAGCTAAGAGAA 2343  
 QY 116 rGlnLeuAsg1yAlaIleG1yGlnMetAspAsnGlnAlaSerGlnLeuThrSerG1ule 136  
 Db 2342 GAGAAATGAAGCTCAGAGACTCTGAGCTCTCCCAAGAACTCGATGACCTTCTGGACCT 2283  
 QY 136 uLYsPheIleLYsAsnAlaValAlaG1yValArgG1yThr----- 149  
 Db 2282 GAACAACCTCAAGTCCAGAGCTTGAACGAGAGAAACACAGCCTTCATTCAGTGAAG 2223  
 QY 149 ----- 149  
 Db 2222 ACTCCAGAGAGAGTGAAGAGCTGTGATGAGCTACACGTGTCCAAGCGCTCCAGATG 2163  
 QY 150 -----Glusterlyse11eTyrLeuValLysG1 159  
 Db 2162 TAACAGTGGCCGTGAGAGTGGCTCAACTTCAGAGAGAGTGTACTTCTGGCGAGGA 2103  
 QY 159 uGluYsArgTyrAlaAspAlaGlnLeuSerCyseGlnGlyArgGlyGlyThrLeuSerMe 179  
 Db 2102 GCCCAAGAGTGGATCCAGGCGCGGTTGGCTGCGACAGAGCTGCAAGGCGCGTGGCCAG 2043  
 QY 179 tProLYsAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnLysGlyLeuAl 199  
 Db 2042 CATCCACAGCAGCAAGAGAGAGAGCTTCCTGGCCAGGATGCAACAAGAGGCGC----- 1988  
 QY 199 aArgValPheIleGlyIleAsnAspLeuGluYsG1yAlaPheValTyrSerAspH1 219  
 Db 1987 ----ACCTGAGATTGGCTCCGCGGACCTGGACAGAGAGGAGGAGTTTATCTGGATGAGCA 1932  
 QY 219 sSerProMetArgThrPheAsnLysTyrPArgSerGlyGluProAsnAsnAlaTyrAspG1 239  
 Db 1931 GAACCCCTG---AACTATAGCAACTGGCGGCGCGGAGGCCCAACACGGGGCGCAGGG 1875  
 QY 239 uGluAspCyseValGlnMetValAlaSerGlyGlyTyrPAsnAspValAlaCyseHisThrTh 259  
 Db 1874 CGAGGACTGCGTGTATGATGACAGGCGCTCGGGCAGTGAATGACCGCTTCTGGCGAGCTC 1815  
 QY 259 rMet 260  
 Db 1814 GCTG 1811

## RESULT 9

US-09-227-357-51  
 ; Sequence 51, Application US/09227357  
 ; Patent No. 6342581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fiescher et al.  
 ; TITLE OF INVENTION: 123 Human Secreted Proteins  
 ; FILE REFERENCE: P2010P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,357  
 ; CURRENT FILING DATE: 1999-01-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684  
 ; EARLIER FILING DATE: 1998-07-07  
 ; EARLIER APPLICATION NUMBER: 60/051,926  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,793  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,925  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,929  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,803  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,732  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,931  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,932  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,916



EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.10  
SEQ ID NO 51  
LENGTH: 1333  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (485)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (486)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (493)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (496)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (587)  
OTHER INFORMATION: n equals a,t,g, or c

FEATURE:  
NAME/KEY: SITE  
LOCATION: (633)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (1330)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-227-357-51  
Alignment Scores:  
Pred. No.: 2,35e-13 Length: 1333  
Score: 222.50 Matches: 56  
Percent Similarity: 48.18% Conservative: 10  
Best Local Similarity: 40.88% Mismatches: 40  
Query Match: 15.44% Indels: 31  
DB: 3 Gaps: 6  
US-09-806-277a-6 (1-271) x US-09-227-357-51 (1-1333)  
Qy 2 ArgglyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuPro 21  
Db 161 CGGGTATAT---CACTGAAAGAGAGAACTACTCCCCAGGTATATCTGCAGCATTCCT 217  
Qy 22 SerglyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValProGly 41  
Db 218 ---GGCTTGCTTGACCTCCAGGGCCC-----CCTGGA 247  
Qy 42 LeuLygIAspAlaGlyGlyValGlyAspIleGlyAlaProGlyArgProGlyArgVal 61  
Db 248 GCAATGATTCCTCCCTGGGCCCCCATGTCATCGGCTTCAGAGAGATGTAAGAC 307  
Qy 62 GlyProThrGlyGlyValGlyAsp----- 69  
Db 308 GCACAGAAAGAGAGAAAGTGAAGAAAGCACTGAGATTGAGATTAAGACTGACCG 367  
Qy 70 MetGlyAspIleGlyGlyValGlySerValGlyArgHisGlyValGlyProIleGly 89  
Db 368 CTAGTCTTGCCCGGTGAAGAGGAGCCAGAGAGAGACTGGAGAAAGAGACCAATGAGA 427  
Qy 90 SerLygIleGlyValGlyAspSerGlyAspIleGlyProProGlyProAsnGly----- 107  
Db 428 CCAAGAGAGAGAGAGAGAGAGTGAATGCTCTCTGACCAAGAGAGACACNNA 487  
Qy 108 -----GluProGlyLeuPro-----CysGlyCysSerGlnLeu 118  
Db 488 TGATANTCTGGAACCGGGGCTGCTGAGTTGACATGTGGAAGCATC 538  
RESULT 10  
US-09-535-521-19  
; Sequence 19, Application US/09535521  
; Patent No. 6410714  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eric R.  
; APPLICANT: McCall, Catherine A.  
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGF RECEPTOR (CANINE CD23)  
; FILE REFERENCE: AL-5  
; CURRENT APPLICATION NUMBER: US/09/535,521  
; EARLIER FILING DATE: 2000-03-24  
; EARLIER APPLICATION NUMBER: 60/125,913  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 624  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ..(624)  
US-09-535-521-19

## Alignment Scores:

Pred. No.: 2,63e-13 Length: 624  
 Score: 217.50 Matches: 52  
 Percent Similarity: 41.92% Conservative: 31  
 Best Local Similarity: 26.26% Mismatches: 73  
 Query Match: 15.09% Indels: 42  
 DB: 4 Gaps: 3

US-09-806-277a-6 (1-271) x US-09-535-521-19 (1-624)

QY 101 GLYProProGlyProAhnGlyGluProGlyLeuPro-CysGluCysSerGlnLeuArgly 120  
 DB 12 GGGTGGCCAGGTGTCAAGACATGAAGAAATCCAACTGAACAGAGAAATGAAGC 71  
 QY 120 sAlaIleGlyGluMeCAspAhnGlnValSerGlnLeuThrSerGlnLeuLysPheIlely 140  
 DB 72 TCAGAGCTGTGAGCTCTCCAGAACCTGTGATGACCTTGTTGGACCTGAACAACCTCA 131  
 QY 140 sAenAlaValAlaGlyValArgGluThr----- 149  
 DB 132 GTCCAGAGCTTGAACAGAGAACACAGCCTTGATTCATCTGAGAGACTCCAGAGGA 191  
 QY 149 ----- 149  
 DB 192 GGTGAGAAAGCTGTGATGAGACTACAGCTGCCAGCTCCAGTGTAAACAGTCCC 251  
 QY 150 -----GluSerIleIleTyrlleuLeuValIysGlnGluLysArgly 163  
 DB 252 TGAGAAAGTGTCACTTCCAGAGAAAGTGTCTACTTCCGCGAGAGGCCCAAGATG 311  
 QY 163 rAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetProLysAspG 183  
 DB 312 GATCCAGGCGCGGTTGGCTGTGACAGAACAGTGCAGAGGGCGGTGGCCAGCATCCACGCCA 371  
 QY 183 uAlaAlaAsnGlyLeuMetAlaIleTyrlleuAlaGlnAlaGlyLeuAlaArgValPheI 203  
 DB 372 AGAGAGAGAGAGACTTCTGCGCGAGGTATGCCAACAGAGAGGC-----ACCTGGAT 422  
 QY 203 eGlyIleAsnAspLeuGlnGlyGlyAlaPheValIleTyrlleuSerPheIleSerPheMet 223  
 DB 423 TGGCTCCGCGGAGCTGTGACAGAGGGGAGTATTCGTGATGACAGAGAACCCCTCG-- 480  
 QY 223 gThrPheAsnLysTrpArgSerGlyGluProAsnAsnAlaTyrlleuAspGlnGluAspCysVa 243  
 DB 481 -AACTATGCAACTGCGCGCGCGGAGCCCAACAACGCGGCGCAGAGGCGAGGACTGCGT 539  
 QY 243 lGluMetValAlaSerGlyGlyTrpAsnAspValAlaCysHisThrThreMet 260  
 DB 540 GATGATGACAGGCTCGGGGAGTGAATGACGCTTGTGCGGAGCTCGCTG 591

## RESULT 11

US-09-535-521-21/c  
 Sequence 21, Application US/09535521  
 Patent No. 6410714

## GENERAL INFORMATION:

APPLICANT: Weber, Eric R.  
 TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)

FILE REFERENCE: AL-5  
 CURRENT APPLICATION NUMBER: US/09/535,521  
 EARLIER FILING DATE: 2000-03-24  
 EARLIER APPLICATION NUMBER: 60/125,913

NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: Patent Ver. 2.1

SEQ ID NO 21  
 LENGTH: 624

TYPE: DNA  
 ORGANISM: Canis familiaris

US-09-535-521-21

## Alignment Scores:

Pred. No.: 2.63e-13 Length: 624  
 Score: 217.50 Matches: 52  
 Percent Similarity: 41.92% Conservative: 31  
 Best Local Similarity: 26.26% Mismatches: 73  
 Query Match: 15.09% Indels: 42  
 DB: 4 Gaps: 3

US-09-806-277a-6 (1-271) x US-09-535-521-21 (1-624)

QY 101 GLYProProGlyProAhnGlyGluProGlyLeuPro-CysGluCysSerGlnLeuArgly 120  
 DB 613 GGGTGGCCAGGTGTCAAGACATGAAGAAATCCAACTGAACAGAGAAATGAAGC 554  
 QY 120 sAlaIleGlyGluMeCAspAhnGlnValSerGlnLeuThrSerGlnLeuLysPheIlely 140  
 DB 553 TCAGAGCTGTGAGCTCTCCAGAACCTGTGATGACCTTGTTGGACCTGAACAACCTCA 494  
 QY 140 sAenAlaValAlaGlyValArgGluThr----- 149  
 DB 493 GTCCAGAGCTTGAACAGAGAACACAGCCTTGATTCATCTGAGAGACTCCAGAGGA 434  
 QY 149 ----- 149  
 DB 433 GGTGAGAAAGCTGTGATGAGACTACAGCTGCCAGCTCCAGTGTAAACAGTCCC 374  
 QY 150 -----GluSerIleIleTyrlleuLeuValIysGlnGluLysArgly 163  
 DB 373 TGAGAAAGTGTCACTTCCAGAGAAAGTGTCTACTTCCGCGAGAGGCCCAAGATG 314  
 QY 163 rAlaAspAlaGlnLeuSerCysGlnGlyArgGlyGlyThrLeuSerMetProLysAspG 183  
 DB 313 GATCCAGGCGCGGTTGGCTGTGACAGAACAGTGCAGAGGGCGGTGGCCAGCATCCACGCCA 254  
 QY 183 uAlaAlaAsnGlyLeuMetAlaIleTyrlleuAlaGlnAlaGlyLeuAlaArgValPheI 203  
 DB 253 AGAGAGAGAGAGACTTCTGCGCGAGGTATGCCAACAGAGAGGC-----ACCTGGAT 203  
 QY 203 eGlyIleAsnAspLeuGlnGlyGlyAlaPheValIleTyrlleuSerPheIleSerPheMet 223  
 DB 202 TGGCTCCGCGGAGCTGTGACAGAGGGGAGTATTCGTGATGACAGAGAACCCCTCG-- 145  
 QY 223 gThrPheAsnLysTrpArgSerGlyGluProAsnAsnAlaTyrlleuAspGlnGluAspCysVa 243  
 DB 144 -AACTATGCAACTGCGCGCGCGGAGCCCAACAACGCGGCGCAGAGGCGAGGACTGCGT 86  
 QY 243 lGluMetValAlaSerGlyGlyTrpAsnAspValAlaCysHisThrThreMet 260  
 DB 85 GATGATGACAGGCTCGGGGAGTGAATGACGCTTGTGCGGAGCTCGCTG 34

## RESULT 12

US-09-795-061-1  
 Sequence 1, Application US/09795061  
 Patent No. 6759528

## GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S  
 TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes

FILE REFERENCE: 960296, 96781  
 CURRENT APPLICATION NUMBER: US/09/795,061  
 EARLIER FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: Patent Ver. 2.1

SEQ ID NO 1  
 LENGTH: 6109

TYPE: DNA  
 ORGANISM: Mus musculus

FEATURE:  
 NAME/KEY: CDS

LOCATION: (82)..(5298)  
 US-09-795-061-1

## Alignment Scores:

Pred. No.: 2.06e-11 Length: 6109

Score: 212.50 Matches: 55  
Percent Similarity: 44.59% Conservative: 15  
Best Local Similarity: 35.03% Mismatches: 51  
Query Match: 14.75% Indels: 37  
DB: 4 Gaps: 4

US-09-806-277a-6 (1-271) x US-09-795-061-1 (1-6109)

Qy 23 GlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValProGlyLeu 42  
Db 4213 GGCCCTCCAGAGGCCCTCGGCCACCTGCGC-----CTCCCTGGGCTG 4254

Qy 43 LysGlyAspAlaGlyGlyLeuGlyAspIlySerGlyAlaProGlyArgProGlyArgValGly 62  
Db 4255 AAGGAGAGTGTCTGGCCCCAAGAGGAGAGAGGCCCATTTGGCTAAATAGGCTCATTTGGT 4314

Qy 63 ProThrGlyIuLySGlyAspMetGlyAspIlyS----- 73  
Db 4315 CCCCCAGGAGAGCCCGGTGAGAAAGCCATCAGGGGTTGCCAGGTGTGAGAGGCCCA 4374

Qy 74 -----GlyGlnLySGlySerValGlyArg 81  
Db 4375 GGCTTTCAGGAGACCTGTCTCTCCGTCTGTGCTGTGCTGTATGATCACCTGGAGCC 4434

Qy 82 HisGlyIlySerIleGlyProIleGlySerIlySGlyIuLySGlyAsp----- 96  
Db 4435 CCAGGTGTGGGCGCCCTCTGTGAGACAGAAAGGCTCCAAAGGATCCCGGATCTTTGGT 4494

Qy 97 ---SerGlyAspIleGlyProProGlyProAsnGlyIuProGlyLeuProCysGlyCys 115  
Db 4495 CCTGTGTGAGACCTGTGAGACAGGAGGCTCTCTGTCTCCCGGGTTCTCCGGTGAAGTG 4554

Qy 116 SerGlnLeuArgIlyS-----AlaIleGlyIuMetAspAsnGlnValSerGlnLeu 132  
Db 4555 CATGAGCTGCGCAGGCGCGCATCTGTGACGACACCTGGAAGGTGGCTGAGAGAGTG 4614

Qy 133 ThrSerGlnLeuIysPheIleYAsnAlaValAlaGlyValArgGlnThr 149  
Db 4615 ATGGCTTCACGTGA-TTCACTGAGCTTGAGCTGACAGATTGACAGAGACC 4664

RESULT 13  
US-09-795-061-3  
Sequence 3, Application US/09795061  
Patent No. 6759528  
GENERAL INFORMATION:  
APPLICANT: Greenspan, Daniel S  
APPLICANT: Imamura, Yasutada  
TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes  
FILE REFERENCE: 960296.96781  
CURRENT APPLICATION NUMBER: US/09/795.061  
CURRENT FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 6200  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (87)..(5321)  
US-09-795-061-3

Alignment Scores:  
Pred. No.: 2,37e-11 Length: 6200  
Score: 212.00 Matches: 54  
Percent Similarity: 43.33% Conservative: 11  
Best Local Similarity: 36.00% Mismatches: 41  
Query Match: 14.71% Indels: 44  
DB: 4 Gaps: 5

US-09-806-277a-6 (1-271) x US-09-795-061-3 (1-6200)

Qy 23 GlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValProGlyLeu 42

Db 4221 GGCCCTCTGTGCGCCCTCGGGGCTCTGGC-----CTCCAGAGGCTG 4262

Qy 43 LysGlyAspAlaGlyGlyIuLySGlyAspIlySerGlyAlaProGlyArgProGlyArgValGly 62  
Db 4263 AAGGAGACACTGGCCCCAAGAGGAGAGAGGCCCATTTGATTTGATGCTCATTTGGC 4322

Qy 63 ProThrGlyIuLySGlyAspMetGlyAspIlyS----- 73  
Db 4323 CCCCCGAGAGAGCTGTGAGAAAGATCAGGGGTTGCCAGGCGTGCAGGAGCCCT 4382

Qy 74 GlyGlnLySGlySerValGlyArgHisGlyIlySerIle----- 85  
Db 4383 GTCTCCAAAGGAGACCTGTGCTCCCTGTGTCCATTGGCTTCTGGGCACTGGGCCC 4442

Qy 86 -----GlyProIleGlySerIlySGlyIuLySGlyAsp----- 96  
Db 4443 CCAGGTGTGGGCGCCCTCTGTGAGACAGAAAGCTCAAAAGGCTCCGGGGTCCATGGGC 4502

Qy 97 ---SerGlyAspIleGlyProProGlyProAsnGlyIuProGlyLeuProCysGlyCys 115  
Db 4503 CCCCCTGAGACACTGAGACTGACAGGCCACAGGCCCCCGGGTGTCCCTGCCAGAGCTG 4562

Qy 116 SerGlnLeuArgIlyS-----AlaIleGlyIu 124  
Db 4563 CATGGCTGCGCAGGCGCGCGCTTGTCTCCAGTCCCGCTTCCAGTGTGAGAGGCGGC 4622

Qy 125 MetAspAsnGlnValSerGlnLeuThrSer 134  
Db 4623 CTGAGAGAGTGTGGCTGCGCTGCTCATCATCG 4652

RESULT 14  
US-09-620-312D-110  
Sequence 110, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Weinman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yundong  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghaast  
APPLICANT: Drmanac, Radjole T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
FILE REFERENCE: Polypeptides  
FILE REFERENCE: 784CIP28  
CURRENT APPLICATION NUMBER: US/09/620.312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: PL\_FL\_genes Version 1.0  
SEQ ID NO 110  
LENGTH: 6674  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1312)..(6330)  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (1) --(6674)  
OTHER INFORMATION: n = a, t, c or g  
US-09-620-312D-110

## Alignment Scores:

Align. No.: 3,73e-11 Length: 6674  
Score: 210.50 Matches: 46  
Percent Similarity: 44.54% Conservative: 7  
Best Local Similarity: 38.66% Mismatches: 31  
Query Match: 14.61% Indels: 35  
DB: 4 Gaps: 2

US-09-806-277A-6 (1-271) x US-09-620-312D-110 (1-6674)

QY 23 GYHISProGInProAlaGlyAspAspAlaCySerValGlnIleuValProGlyLeu 42  
DB 4654 GGGCTTACCTGGAGAAAAAGGTGACAAAGC-----CTCCCGGATTG 4695  
QY 43 LysGlyAspAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
DB 4696 GATGGCATCCCTGGATGTCACAAAGAGACAGAGCTTCTGAGACTCTGGCCACAGGC 4755  
QY 63 ProThrGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 69  
DB 4756 CCAGCTGGCCAGAAAGGGAGCCAGCAGTATGTAATCCCGGGGTGACAGAGAGAG 4815  
QY 70 -----MetGlyAspLys 73  
DB 4816 GGTGAACAGGTCTACAGAGAGAGATTCACAGGTTTCCAGGGCCAAAGAGAGAGAG 4875  
QY 74 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 93  
DB 4876 GGTTCAAAGGTGAGGTGGTTCCTCCAGAGATTACCGGAGCCAGAGATTCCTGATCC 4935  
QY 94 LysGlyAspSerGlyAspIleGlyProProGlyProAsnGlyGlyGlyGlyGlyGly 112  
DB 4936 AAAGAGAGAGCAAGATTCATGGTCTCCGGGCCCCAGGAGACAGCCGGGTTACCG 4992

## RESULT 15

US-09-919-497-6  
Sequence 6, Application US/09919497  
Patent No. 6773883  
GENERAL INFORMATION:  
APPLICANT: Muter, George L.  
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER  
FILE REFERENCE: B0801/7225  
CURRENT APPLICATION NUMBER: US/09/919,497  
PRIORITY FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: US 60/221,735  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 6158  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Unsure  
LOCATION: (2434) ..(2434)  
OTHER INFORMATION: n = a, c, g or t/u  
US-09-919-497-6

## Alignment Scores:

Align. No.: 3,75e-11 Length: 6158  
Score: 210.00 Matches: 81  
Percent Similarity: 34.11% Conservative: 36  
Best Local Similarity: 23.62% Mismatches: 100  
Query Match: 14.57% Indels: 126  
DB: 4 Gaps: 13

US-09-806-277A-6 (1-271) x US-09-919-497-6 (1-6158)

QY 23 GlyHisProGInProAlaGlyAspAspAlaCySerValGlnIleuValProGlyLeu 42

DB 4446 GAGACACCTGGTCTTATGGAGACTCTCTGC-----TTACTGATCTC 4487  
QY 43 LysGlyAspAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
DB 4488 AAAGTACCTGGCTCCCAAGGGGTGAAAAGGACATCTGTATTATGCTGATTTGGT 4547  
QY 63 ProThrGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 73  
DB 4548 CTTCCAGAGAGAAAGGGAGAAAAGGTGACCGAGGCTCTCCGAACTCAAGATCTCCA 4607  
QY 74 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 88  
DB 4608 GAGAGAAAAGGGAGATGGGGAATTCCTGGTCTCGTGTCTCTAGTCCACCTGGTCTC 4667  
QY 89 -----GlySerLysGly 92  
DB 4668 CCAGCTTACAGGCTCTCAAGGCCCAAGGGTACAAAGCTTACCTGAGACCGCTGC 4727  
QY 93 GlyLysGlyAspSerGlyAspIleGlyProProGlyProAsnGlyGlyGlyGlyGly 110  
DB 4728 CAGAAAGTGAAGTGTGCTTCCAGGGCTCTGGGCTTCAGGTCACCTGATGAATC 4787  
QY 111 -----LeuProCysGlyCysSerGln 117  
DB 4788 ATTCAAGCTTTACCATCTTGTCTCCAAAAGAGAGACATCTGAAGCATGCA 4847  
QY 118 -----LeuArgLysAlaIleGlyGly 124  
DB 4848 GCAGATGACAGATGATATATCTTGATCTCTCGATGAGATGAGAAATATTTGGTCC 4907  
QY 125 MetAspAsnGlnValSerGlnLeuThrSerGlyLeuLysPheIleValAsnAlaVal 144  
DB 4908 CTC--AATTCCTGAAACAGACATCGACATATGAATTTCCATGGTACTCAGACC 4964  
QY 145 GlyValArgGlyThrGlySerLysIleTyrLeuLeu-----ValLysGlyGlyLys 161  
DB 4965 AATCCAGCCCACTGTAAAGACCTGCAACTCAGCATCTGATCTCCAGATGGTGA 5024  
QY 162 ArgTyrAlaAspAlaGlnLeuSerCysGlyGly----- 172  
DB 5025 TATTGATTGATCTTACCAAGGTTCCTCAGAGATTCCTCAAGTTACTGTAATTTTC 5084  
QY 173 ---ArgGlyGlyThrLeuSerMetProLysAspGlyAlaIleAsnGlyLeuMetAla 191  
DB 5085 ACATCTGGTGTGAGACTTGCAATTTATCCAGAAAAAATCTGAGGA----- 5132  
QY 192 TyrLeuAlaGlnAlaGlyLeuAlaArgValPheIleGlyIleAsnAspLeuGlyGly 211  
DB 5133 -----GTAAGAATTTCAATCATGCGCCAAAGAG 5159  
QY 212 GlyAlaPheValTyrSerAspHisSerPrometArgThrPheAsnLysTyrAspSerGly 231  
DB 5160 -----AAACGAGAGATTGGTTTATGTAATTTAAGAGGGA 5195  
QY 232 GluProAsnAsnAlaTyrAsp---GluLysAspCysValGluMetVal----- 246  
DB 5196 AATCGCTTTCATCTTAACTGATGTTGAAGAAATTCATCAATATGTGTGAATGACATTC 5255  
QY 247 -----AlaSerGly 249  
DB 5256 CTGAACCTTCTGACTGCTCTGCTCGCAAAATTTACCTACCTACCTGATCAGCA 5315  
QY 250 GlyTyrAspAspValAlaCysHisThr-----ThrMetLysPheMetCysGlyPhe 266  
DB 5316 GCCTGTGATGATGTGATCAGAGAAATTTATGACAAAGCACTTGCTTCTGGGATCAAT 5375  
QY 267 AspLysGlyLys 269  
DB 5376 GATGAGAG 5384

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Mon Dec 20 08:22:14 2004

us-09-806-277a-6.rn1

Page 11

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 03:40:34 ; Search time 5448 Seconds

(without alignments)  
2352.333 Million cell updates/sec

Title: US-09-806-277a-6

Perfect score: 1441

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9083458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=genembl -QMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=spct -THR MAX=100 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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13: gp\_un.\*  
14: gp\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	813	BD103332	Novel col
2	1441	100.0	1238	AR252616	Sequence
3	1441	100.0	1238	AX403469	Sequence
4	1441	100.0	1238	AX454582	Sequence

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BD103332	Novel collectin.	BD103332.1 GI:22648906	BD103332.1	GI:22648906	Novel collectin	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 813)	Wakamiya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.	Novel collectin	Patent: WO 0181401-A 31 01-NOV-2001; FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI	OS Homo sapiens (human) PN WO 0181401-A/31 PD 01-NOV-2001 PF 23-APR-2001 WO 2001JP003468 PR 21-APR-2000 JP 00P 120358 PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI
AX491060	Sequence	AX491060	AX491060	AX491060	Sequence	Mus muscu	AC123656	AC123656	Mus muscu	AC123656	AC123656	AC123656

ALIGNMENTS

813 bp DNA linear PAT 27-AUG-2002

Location/Qualifiers

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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
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 Pred. No.: 1,286-86 Length: 813  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 61 CCATCTGGAACATCTCTCAAGCCGGCTGGCGATGACCCCTGCTGTGCAAGATCTGCTCCT 120  
 QY 41 GlyLeuLysGlyAspAlaGlyGluLysGlyAspLysGlyAlaProGlyIaTyrProGlyIaArg 60  
 Db 121 GGCTCTCAAGGGGATGCGGGAGAGAAAGGAGACAAAGCGCCCGGACGGCTGGAAGA 180  
 QY 61 ValGlyProThrGlyGluLysGlyAspMetGlyAspLysGlyGluLysGlySerValGly 80  
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 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGluLysGlyAspSerGlyAspIle 100  
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 Db 301 GGAACCCCTGGTCTTAATGAGAACCAAGGCTCCCATGTGATGACACCGCTGGCAAG 360  
 QY 121 AlaIleGlyIleMetAspAsnGlnValSerGlnLeuThrSerGluLeuLysPheIleLys 140  
 Db 361 GCCATCGGGAGATGACAAACAGGCTCTCTAGCTGACCAAGCAAGCTCAAGTTCATCAAG 420  
 QY 141 AsnAlaValAlaGlyValaArgGluThrGluSerLysIleTyrLeuLeuValLysGluGlu 160  
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 Db 481 AAGGCTACAGCGGAGCGCGAGCTGTCTGCGCAGGGCGCGGAGGAGCATGAGATCCCC 540  
 QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaIleTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
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 QY 241 AspCysValaGluMetValaIaSerGlyGlyTyrAsnAspValaIaCysHisIleThrThMet 260  
 Db 721 GACTGCTGAGATGATGAGCTCGGGCGGCTGGAACGAGTGGCTGCAACACCAATG 780  
 QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271

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 DEFINITION AR252616  
 ACCESSION AR252616  
 VERSION AR252616.1 GI:27300524  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1238)  
 AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.  
 TITLE Implant, method of making same and use of the implant for the  
 treatment of bone defects  
 Patent: US 6478825-A 356 12-NOV-2002;  
 JOURNAL Location/Qualifiers  
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 source /organism="unknown"  
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 Alignment Scores:  
 Pred. No.: 1,986-86 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0  
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 QY 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
 Db 67 ATAGAGGGGGAATCTGGCCCTGGTGGCGTCTTAATCAAGCCCTGCTCTGCACTGCTG 126  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCATCTGGAACATCTCTCAAGCCGGCTGGCGATGACCCCTGCTGTGCAAGATCTGCTCCT 186  
 QY 41 GlyLeuLysGlyAspAlaGlyGluLysGlyAspLysGlyAlaProGlyIaTyrProGlyIaArg 60  
 Db 187 GGCTCTCAAGGGGATGCGGGAGAGAAAGGAGACAAAGGCGCCCGGACGGCTGGAAGA 246  
 QY 61 ValGlyProThrGlyGluLysGlyAspMetGlyAspLysGlyGluLysGlySerValGly 80  
 Db 247 GTCCGGCCCAAGGAGAAAGAGACATGGGGACAAAGGACAAAGGACAGTGGGT 306  
 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGluLysGlyAspSerGlyAspIle 100  
 Db 307 CGTATGGAAGAAATTGGTCCCATTTGGCTCTTAAGTGAAGAAAGAGATTCCGGTGAATA 366  
 QY 101 GlyProProGlyProAlaGlyGluProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
 Db 367 GGAACCCCTGGTCTTAATGAGAACCAAGGCTCCCATGTGATGACAGCGCTGGCAAG 426  
 QY 121 AlaIleGlyIleMetAspAsnGlnValSerGlnLeuThrSerGluLeuLysPheIleLys 140  
 Db 427 GCATCGGGAGATGACAAACAGGCTCTCACTACCAACAGCGAGCTCAAGTTCATCAAG 486  
 QY 141 AsnAlaValAlaGlyValaArgGluThrGluSerLysIleTyrLeuLeuValLysGluGlu 160  
 Db 487 AATGCTGTCCGCGGTGTGGCGGAGACAGCAAGATCTAATCTGCTGTGTAAGAGAGAG 546  
 QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyIaTyrGlyIaTyrLeuSerMetPro 180  
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 QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaIleTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
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QY 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCATCGGCATCAAGACCTGAGAGAGGGCGCTTCGTACTCTGACCACTCC 726  
QY 221 PrometArGTThrPheAsnLysTrpArgSerGlyGluProAsnAsnAlaTyrAspGlu 240  
Db 727 CCCATCGGACCTTCAACAAAGTGGCGACGGCTGAGCCCAACATGCTTACAGAGAG 786  
QY 241 AspCyValGluMetValAlaSerGlyGlyTrpAsnAspValAlaCyAsHisThrMet 260  
Db 787 GACTGCGGAGATGTGTGGCTCGGCGGCTGGAACGACGTGCTGCACACCACTCATG 846  
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RESULT 3  
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LOCUS Sequence 356 from Patent WO0073454.  
ACCESSION AX403469  
VERSION AX403469.1 GI:21436970  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1  
Ferrara N., Baker K.P., Botstein D., Desnovers L., Eaton D.,  
Ferrara N., Gerber H., Gerritsen M., Goddard A., Godowski P.,  
Grimaldi C.J., Gurney A.L., Kijavlin I., Napier M.A., Pan J.,  
Paoni N.F., Roy M., Stewart T.A., Tumas D., Watanabe C.K.,  
Williams P., Wood W.I. and Zhang Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0073454-A 356 07-DEC-2000;  
Genentech Inc. (US)

JOURNAL  
Genentech Inc. (US)

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Source location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Pred. No.: 1.98e-86 Length: 1238  
Score: 1441.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x AX403469 (1-1238)

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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 127 CCATCTGGAACATCCCAAGCCGCTGGCATGACGCTGCTCTGTCACATCTCTCCCT 186  
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60  
Db 187 GGCCTCAAAAGGGATGCGGAGAGAAAGGAGCAAAAGCGCCCGGAGCGGCTTGAGAGA 246  
QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
Db 247 GTCCGCCCCACGGGAGAAAGAGACATGGGGGCAAAAGACAGAAAGGCGGTGGGT 306  
QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
Db 307 CGTCAATGAAAAAATGTGCTCCATTTGGCTTAAGGTGAGAAAGAGATTCCGGGTGACATA 366

QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyGlyCysSerGlnLeuArgLys 120  
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QY 121 AlaIleGlyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
Db 427 GCCATCGGAGAGAGCAACAGAGCTCTGAGTACACAGAGCTCAAGTTCTATCAAG 486  
QY 141 AsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValLysGlu 160  
Db 487 AATGCTGTCCCGGTGTGCCGAGACCGAGAGCAAGATCTACTCTGCTGTGAAGAGAG 546  
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QY 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 607 AAGACGAGGCTGCCAATGGCTGATGGCCATACCTGGCGCAAGCGGCTGGCCCT 666  
QY 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
Db 667 GTCTTCATCGGCATCAAGACCTGAGAGAGGGCGCTTCGTACTCTGACCACTCC 726  
QY 221 PrometArGTThrPheAsnLysTrpArgSerGlyGluProAsnAsnAlaTyrAspGlu 240  
Db 727 CCCATCGGACCTTCAACAAAGTGGCGACGGCTGAGCCCAACATGCTTACAGAGAG 786  
QY 241 AspCyValGluMetValAlaSerGlyGlyTrpAsnAspValAlaCyAsHisThrMet 260  
Db 787 GACTGCGGAGATGTGTGGCTCGGCGGCTGGAACGACGTGCTGCACACCACTCATG 846  
QY 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 847 TACTTCATGTGTGAGTTTGACAAAGAAACATG 879

RESULT 4  
AX454582 1238 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 167 from Patent WO0208284.  
ACCESSION AX454582  
VERSION AX454582.1 GI:21713915  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1  
Baker K.P., Ferrara N., Gerber H., Gerritsen M.E., Goddard A.,  
Godowski P.U., Gurney A.L., Hillan K.J., Marsters S.A., Pan J.,  
Paoni N.F., Stephan J.P., Watanabe C.K., Williams P.M., Wood W.I.  
and Ye W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0208284-A 167 31-JUN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

JOURNAL  
Genentech, Inc. (US)

FEATURES  
Source location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Pred. No.: 1.98e-86 Length: 1238  
Score: 1441.00 Matches: 271

Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 6  
 Gaps: 0  
 Conservative: 0  
 Mismatches: 0  
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US-09-806-277a-6 (1-271) x AX454582 (1-1238)

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 Db CCATCTGACATCTCTCAGCCGCTGGCGATGACCCCTGCTGCTGCTGCTGCTGCT 186  
 QY 41 GlyLeuLysGlyAspAlaGlyValGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60  
 Db GGCTCAAGAGGAGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
 QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
 Db GTGGGCCCCAGGAG 306  
 QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyLysGlyAspSerGlyAspIle 100  
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 QY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
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 QY 141 AsnAlaValAlaGlyValArgGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 160  
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 QY 181 LysAspGlyLysAlaAsnGlyLysMetAlaAlaTyrLeuValGlnIleValArg 200  
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 QY 201 ValPheIleGlyLysAsnAspLeuGlyLysGlyLysGlyLysGlyLysGlyLys 220  
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 Db TACTTCATGTGTGATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879  
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 AX491060 1238 bp DNA linear PAT 16-AUG-2002  
 LOCUS AX491060  
 DEFINITION Sequence 167 from Patent WO0200690.  
 ACCESSION AX491060  
 VERSION AX491060.1 GI:22323867  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Baker, K.P., Ferrera, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
 Pooni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
 and Ye, W.  
 Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0200690-A 167 03-JAN-2002;  
 Genentech, Inc. (US)

TITLE  
 JOURNAL  
 FEATURES  
 source  
 location/Qualifiers  
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## ORIGIN

## Alignment Scores:

Pred. No.: 1,98e-86 Length: 1238  
 Score: 1441.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 DB: 6 Gaps: 0

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 Db GTCTTCATCGGATCAAG 726  
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Db 727 CCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACATGCTTACGACGAGAG 786  
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 LOCUS AY358439 Homo sapiens clone DNA59848 RGNL596 (UNQ596) mRNA, complete cds.  
 ACCESSION AY358439.1 GI:37182002  
 VERSION AY358439.1  
 KEYWORDS FLI CDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1238)  
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,  
 Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robble,E., Sanchez,C.,  
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vagstad,A., Vandlen,R., Watanabe,C., Wiesand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.  
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 Genome Res. 13 (10), 2265-2270 (2003)  
 JOURNAL PUBMED 12975309  
 REFERENCE 2 (bases 1 to 1238)  
 Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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 REFERENCE 1 (bases 1 to 1248)  
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
 Klausner,R.D., Collins,F.S., Wagner,L., Shenman,C.M., Schuler,G.D.,  
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

**TITLE**  
 JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL  
 2 (bases 1 to 1248)  
 Straubeberg, R.  
 Direct Submission  
 Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 20, 2003 this sequence version replaced gi:12652660.  
 Contact: MGC help desk  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing By: Institute for Systems Biology  
<http://www.systemsbioology.org>  
 contact: [amadams@systemsbioology.org](mailto:amadams@systemsbioology.org)  
 Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whitting

**REMARK**  
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Contact: nhec\_mgc@hgrl.nih.gov  
 Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
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 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
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 1 (bases 1 to 813)  
 AUTHORS Wakamitsu, N., Keshi, H., Otsu, K., Sakamoto, T. and Kishi, Y.  
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 FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMITSU,  
 KESHI, KATSUKI OTSUKI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
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US-09-806-277A-6 (1-271) X BD103338 (1-813)

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DEFINITION	Novel collection.				
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ORGANISM	Mus musculus				
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AUTHORS	I (bases 1 to 1522)				
TITLE	Wakamaya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.				
JOURNAL	Novel collection				
COMMENT	Patent: WO 0181401-A 6 01-NOV-2001; FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI OS Mus musculus (mouse) PN WO 0181401-A/6 PD 01-NOV-2001 PF 23-APR-2001 WO 2001JP003468 PI 21-APR-2000 JP 00P 120358 PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI SAKAMOTO, PI YUICHIRO KISHI PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53 CC Novel collection FH Key FT CDS Location/Qualifiers Location/Qualifiers 1..1522 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090"				
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QY	21	ProSerGtYhSPProGInPrAlaGlYAsPaSpAlaCySSerValGIhLlaleuValPro	40		
DB	217	CCATTCGTGATGTCTCCACAGCACCAACAGAGACGCCGTGCTGTGCAAAATTCGTCCCC	276		
QY	41	GtYLeuLYSGtYAsPaAlaGlYGlYLeuSgLYAsPySgLYAlAProGLYArGProGLYArG	60		
DB	277	GGCCTCAAAGGGGATGCAGAGAAGGAAGGACAAGAGAGCCCAAGACGGCCAGGAAGA	336		
QY	61	ValGtYProThrGtYGlYLeuSgLYAsPwMetGtYAsPYsGtYGlYLeuSgLYSeValGtY	80		
DB	337	GTCGGCCCTTAAGAGAAAAGAGACATGCGGGGACAAAGAGACAGAAAGGACTGTGGGC	396		
QY	81	ArgHtAgLySvSllegLYProIllegLYSerLYSgLYgluYsgLYAsPSerGtYAsPlle	100		
DB	397	CGCCATGGAAAAATTTGTCCTCAATGGCCCAAAAGGTGAAAAAGGAGATTCTGTGATAATC	456		
QY	101	GtYProPGtYProAsnGtYGlYLPProGtYLeuPProCYsGtYCuYSerGtYLeuArGtYs	120		
DB	457	GGACCCCTGGCCCAAGTGAAGAACCTGTTCATTTGATGTGAGTCAAGTCAAGTGAAGAG	516		
QY	121	AlaileGtYglumeAsPaSnGInVaISerGInLeuThrSerGtYLeuLYsPheIlleYs	140		
DB	517	GCTATTGGGGAGATGACCAACCAAGGTCACTCAACTGACCAACTGAGCTAAATTCATAA	576		
QY	141	AsnaIaVaIlaAGtYValArgGtYhTrhGtYhTrhGtYhTrhGtYhTrhGtYhTrhGtYhTrh	160		



Db	577	AAATGCTGTTCCTGGCTGGCGCAGACTGAGACAGATCTTACCTGCTGTGTAAAGAGAG	636
QY	161	LYBAAGTYRALAASPAIAGINLEUSERCYSGINGIYARGIYGIYTHIRLEUSERMETPRO	180
Db	637	AAGCGGTGCGCAGATGCCAGCTGTCTCCCAAGCCGAGGGCGGCACATGAGCATGGCC	696
QY	181	LYBAAPGIALAIALAASNGIYLEUMETVALAITYRLEUNLAGIAGIYLEUNIAAG	200
Db	657	AAAGCGAGGCGCCCAATGGCTGATGGCTTAATCTTACCTGACAGGCTGGCTGGCCCA	756
QY	201	VALPHEIIEGIYLAASNAAPLEUNGUYSGIUGIYALAPHEVALTYRISERAPHSISER	220
Db	757	GCTTCATCGGTATCAATGACTCGGAGAAAGAGGCTTTGCTGTACTCGAGCGGCTCC	816
QY	221	PROMETARGTHPHEASNLERTTPHARGSERGIYGLUPROASMAASHALARYRSPGIUGLU	240
Db	817	CCCAATGCGACCTTCAACAGATGGCGCAATGGAGAGGCCAACACACCCCTATATATGGAG	876
QY	241	AAPCYVALIGLUETVALAIAASERGIYGIYTPASMAAPVALIAECYSHISTHRTMRET	260
Db	877	GACTGTGTGGAAGATGATGGCTCAGGTGGCTGGAATGATGTGGCTGCGCACTTACCAAG	936
QY	261	TYRPHMETCYSGIUPHEAPSIYSGIUSANMET	271
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RESULT 12.	BD103341				
LOCUS	BD103341	741 bp	DNA	linear	PAT 27-AUG-2001
DEFINITION	Novel collectin.				
ACCESSION	BD103341				
VERSION	BD103341.1	GI:22648915			
KEYWORDS	MO 0181401-A/40.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 741)				
TITLE	Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.				
JOURNAL	Novel collectin				
	Patent: WO 0181401-A 40 01-NOV-2001;				
	FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI				
	KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI				
COMMENT	OS Homo sapiens (human)				
	PN WO 0181401-A/40				
	PD 01-NOV-2001				
	PF 23-APR-2001 WO 2001JP003468				
	PR 21-APR-2000 JP 00P 120358				
	PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI				
	SAKAMOTO,				
	PI YUICHIRO KISHI				
	PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53				
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Best Local Similarity:	91.14%
Query Match:	89.45%
DB:	6
Gaps:	1
length:	741
Matches:	247
Conservative:	0
Mismatches:	0
Indels:	24
Gaps:	1

US-09-806-277A-6 (1-271) X BD103341 (1-741)

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QY 21 ProSerGgiYH1aProGlnProAlaGlyYAspAspA1aCySerValGlnIleLeuValPro 40

Db 61 CCAATCTGAACATCTCTCAACCGGCTGGCGATACCGCTCTCTGTGACAGATCTCTGCTT 120

QY 41 GlyLeuIlysgIYaBPAlaGlyGlyIlysgIlyAspIlysgIyAlaProGlyYArgProGlyArg 60

Db 121 GGCCCTCAAAAGGGGATGCGGGAGAGAAAGGAGCAAAAGCGCCCCCGACCGGCTGGAGAA 180

QY 61 ValGgiProThrGgiYgIlyGlyIlysgIyAspMetGlyAspIlysgIyIlyGlySerValGly 80

Db 181 GTGGCCCCACGGAGAA----- 198

QY 81 ArgH1sgIyYsIlegIyProIlegIySerIlysgIyGlyIlysgIyAspSerGlyYAspIle 100

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QY 101 GlyProProGgiYProAsnGlyGlyIlyProGgiYleuProCyAsgIlyCySerGlnIleuArgIly 120

Db 229 GGACCCCCCTGGTGTCTTAATGAGAAACCAAGGCTCCCATGTGATGTCACAGCACTGGCAAG 288

QY 121 AlaIlegIyGlnMetAspAsnGlnValSerGlnIleuThrSerGlyLeuIlyPheIleIly 140

Db 289 GCCATCGGGGAGATGACACCAAGTCTCTCACTGACACAGCACTCAAGTTCATCAAG 348

QY 141 AsnAlaValAlaGlyValArgIlyIlyThrGlnSerIlyIleYrLeuLeuValIlysgIlyIly 160

Db 349 AATCTGTGCGCGGTGTGCGGAGAACGAGACAAAGATCTACCTGCTGTGAAGAGAG 408

QY 161 LysArgTrpYrAlaAspAlaGlnLeuSerCySerGlnIlyArgGlyIlyThrLeuSerPhePro 180

Db 409 AAGGCGTACGGGAGCGCCCACTGTCTCGCCAGGGCGCGGGGGGACGCTAAGCATGCC 468

QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaIlyrLeuAlaGlnAlaGlyLeuAlaArg 200

Db 469 AAGGACGAGCGTGGCAATGGCTGATGGCGGCATACCTGGCGCAAGCCGGGCTGGCCGCT 528

QY 201 ValPheIlegIyIleAsnAspLeuGlnIlysgIlyGlyAlaPheValYrSerAspH1Ser 220

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QY 241 AspCyValAlaGlnMetValAlaSerGlyGlyYrTrpAsnAspValAlaCyValIleThrMet 260

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RESULT 13	BD103331				
LOCUS	BD103331				
DEFINITION	Novel collectin.				
ACCESSION	BD103331				
VERSION	BD103331.1 GI:22648905				
KEYWORDS	WO 0181401-A/30.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1269)				
TITLE	Wakamaya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.				
JOURNAL	Novel collection				
	Patent: WO 0181401-A 30 01-NOV-2001;				
	FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI				



COMMENT  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PD WO 0181401-A/30  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMITTA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
CC Novel collection  
FH Key location/Qualifiers  
FT CDS (265)..(1005).  
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Alignment Scores:  
Pred. No.: 2,166-76 Length: 1269  
Score: 1289.00 Matches: 247  
Percent Similarity: 91.14% Conservative: 0  
Best Local Similarity: 91.14% Mismatches: 0  
Query Match: 89.45% Indels: 24  
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US-09-806-277A-6 (1-271) x BD103331 (1-1269)  
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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 335 CCATCTGGACATCTCTCAGCCGCGCTGGCCATGACGCTGCTCTGTGCAATCTCTGCTCCT 384  
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyValArgProGlyValArg 60  
DB 385 GGCCTCAAGGGGATGCGGAG 444  
QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysGlySerValGly 80  
DB 445 GTCCGCGCCCAACCGAGAA----- 462  
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DB 463 -----AAAGGTGAGAGAGAGAGATTCCGGTACATTA 492  
QY 101 GlyProProGlyProAsnGlyGlyLysProGlyLysProCysGlyCysSerGlnLeuValArgLys 120  
DB 493 GGAACCCCTGGTCTTAATGAGAGACAGGCTCCCATGTAGTGAAGCAGCTGCGCAG 552  
QY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
DB 553 GCCATCGGGAGATGAGACAAACAGGTCTCTCAGCTGACAGCAGCACTCAAGTTCAATCAAG 612  
QY 141 AsnAlaValAlaGlyValArgGlyLysThrGlySerLysIleTyrLeuLeuValLysGlyLys 160  
DB 613 AATGCTGTGCGCGGTGCGGAG 672  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValArgGlyLysThrLeuSerMetPro 180  
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QY 201 ValPheIleGlyLysAsnAspLeuGlyLysGlyLysAlaPheValTyrSerAspHisSer 220  
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QY 221 PrometArgThrPheAsnLysTyrArgSerGlyGlyLysProAsnAsnAlaIleTyrAspGlyLys 240  
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DB 913 GACTGCGGAGAGATGGGCTCGGGCGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 972  
QY 261 TyrPheMetCysGlyLysPheAspLysGlyLysMet 271  
DB 973 TACTTCACTGTGATGATTGACAGAGAGACATG 1005  
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BD103340  
LOCUS Novel collection.  
DEFINITION Novel collection.  
ACCESSION BD103340  
VERSION BD103340.1 GI:22648914  
KEYWORDS WO 0181401-A/39.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 741)  
AUTHORS Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
PATENT: WO 0181401-A 39 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMITTA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/39  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMITTA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
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Pred. No.: 1,946-76 Length: 741  
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DB: 6 Gaps: 1  
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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 61 CCATCTGGACATCTCTCAGCCGCGCTGGCCATGACGCTGCTCTGTGCAATCTCTGCTCCT 120  
QY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyValArgProGlyValArg 60  
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Db 127 -----AAAGAGACATGGGGGCAAGAGCAAGAAAGGAGTGTGGCT 168  
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Qy 221 PrometArgThrPheAspIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 240  
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DEFINITION BD103330.1 GI:22648904  
ACCESSION WO 0181401-A/29.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1269)  
AUTHORS Makamiya,N., Keshi,H., Ocani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collectin  
JOURNAL Patent: WO 0181401-A 29 01-NOV-2001.  
FISO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PN WO 0181401-A/29  
PD 01-NOV-2001  
PR 23-APR-2001 WO 2001JP003468  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
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ORIGIN

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Pred. No.: 3,4e-76 Length: 1269  
Score: 1286.00 Matches: 247  
Percent Similarity: 91.14% Conservative: 0  
Best Local Similarity: 91.14% Mismatches: 0  
Query Match: 89.24% Indels: 24  
DB: 6 Gaps: 1

US-09-806-277a-6 (1-271) x BD103330 (1-1269)

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Db 325 CCATCTGGAATCTCAGCGCGCTGCGGATGACGCTGCTGTGCAAGATCCTGCTCCT 384  
Qy 41 GlyIleIleGlyIleIleGlyIleIleGlyIleIleGlyIleIleGlyIleIleGlyIle 60  
Db 385 GGCCTC----- 390  
Qy 61 ValGlyProThrGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 80  
Db 391 -----AAAGAGACATGGGGGCAAGAGCAAGAAAGCAATGTGGCT 432  
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Db 433 CGTCATGGAATAATGGTCCCATTTGGCTCTAAAGGTGAGAAAGCAATCCGGTGA 492  
Qy 101 GlyProProGlyProGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 120  
Db 493 GAGCCCCCTGCTCTAATGAGAACCAAGGCTCCATGAGTGAAGCCAGCTGCGCAG 552  
Qy 121 AlaIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 140  
Db 553 GCCATCGGGAGATGAGCAACAGCTCTCAGCTGACCAAGCAAGCTCAATCACTAG 612  
Qy 141 AenAlaValAlaGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 160  
Db 613 AATGCTGTGCGCGGTGTGCGGAGACGAGACAGATCTACTCTGCTGTGAGAGAGAG 672  
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Qy 201 ValPheIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 220  
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Job time : 5456 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 07:12:55 ; Search time 925 Seconds  
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7110.837 Million cell updates/sec

Title: US-09-806-277A-13

Perfect score: 1253  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapect 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

1: \_geneseqn1980a:\*\n2: \_geneseqn1990a:\*\n3: \_geneseqn2000a:\*\n4: \_geneseqn2001a:\*\n5: \_geneseqn2001b:\*\n6: \_geneseqn2002a:\*\n7: \_geneseqn2002b:\*\n8: \_geneseqn2003a:\*\n9: \_geneseqn2003b:\*\n10: \_geneseqn2003c:\*\n11: \_geneseqn2003d:\*\n12: \_geneseqn2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253	100.0	1253	3	AAZ94946 Human car
2	1240.6	99.0	1383	10	AD160324 Secreted
3	1230	98.2	1238	3	AAZ65084 Membrane-
4	1230	98.2	1238	3	AAZ58385 Human PRO
5	1230	98.2	1238	5	AAZ44230 Human PRO
6	1230	98.2	1238	6	ABL88155 Human PRO
7	1230	98.2	1238	6	ABL95644 Human ang
8	1230	98.2	1238	8	ACA64399 Human sec
9	1230	98.2	1238	8	ABX80858 Human sec
10	1230	98.2	1238	8	ACD44367 CDNA enco
11	1230	98.2	1238	8	ABX79538 Human sec
12	1230	98.2	1238	8	ACA93559 Novel hum
13	1230	98.2	1238	8	ABX81241 Novel hum
14	1230	98.2	1238	8	ACA93057 Novel hum
15	1230	98.2	1238	8	ABX17141 Human PRO
16	1230	98.2	1238	9	ACA67996 Novel hum
17	1230	98.2	1238	9	ACA88445 Human sec
18	1230	98.2	1238	9	ACD81952 CDNA enco
19	1230	98.2	1238	9	ADA37867 Human CDN
20	1230	98.2	1238	9	ADA21553 Human CDN
21	1230	98.2	1238	9	ADA10340 Human CDN

22	1230	98.2	1238	9	ADA17884 CDNA enco
23	1230	98.2	1238	9	ADA27892 Human CDN
24	1230	98.2	1238	9	ADA94572 Human CDN
25	1230	98.2	1238	9	ADA38797 Human CDN
26	1230	98.2	1238	9	ADA92918 Human CDN
27	1230	98.2	1238	9	ACH65513 Human CDN
28	1230	98.2	1238	9	ADA22479 Human CDN
29	1230	98.2	1238	9	ACD39503 Human CDN
30	1230	98.2	1238	9	ADA06645 Human sec
31	1230	98.2	1238	9	ADA39338 Human CDN
32	1230	98.2	1238	9	ADB96364 Human PRO
33	1230	98.2	1238	10	ADC57836 Human PRO
34	1230	98.2	1238	10	ADC55200 Human PRO
35	1230	98.2	1238	10	ADC12067 Human CDN
36	1230	98.2	1238	10	ADC56489 Human PRO
37	1230	98.2	1238	10	ADC07544 Human CDN
38	1230	98.2	1238	10	ADC11534 Human CDN
39	1230	98.2	1238	10	ADC14656 Novel hum
40	1230	98.2	1238	10	ADD08188 Novel hum
41	1230	98.2	1238	10	ADC82013 Human PRO
42	1230	98.2	1238	10	ADD07655 Novel hum
43	1230	98.2	1238	10	ADC82546 Human PRO
44	1230	98.2	1238	10	ADD10456 Human sec
45	1230	98.2	1238	10	ADD08726 Novel hum

## ALIGNMENTS

RESULT 1	AAZ94946	standard; CDNA, 1253 BP.
ID	AAZ94946	
AC	AAZ94946	
XX		
DT	01-AUG-2000	(first entry)
XX		
DE	Human carbohydrate-associated protein CRBP-6 CDNA.	
XX		
KW	CRBP-6; carbohydrate-associated protein 6; human; autoimmune disorder;	
KW	inflammation; gastrointestinal disorder; infection;	
KW	reproductive disorder; neurological disorder; eye disorder;	
KW	cell proliferation; cancer; diagnosis; gene therapy; ss.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	90..905
FT		/*tag= a
FT	sig_peptide	90..149
FT		/*tag= b
FT	mat_peptide	150..902
FT		/*tag= c
XX		
PN	WO200018922-A2.	
PD	06-APR-2000.	
XX		
PF	29-SEP-1999;	99WO-US022685.
XX		
PR	01-OCT-1998;	98US-00164785.
PR	01-OCT-1998;	98US-0155267P.
PR	06-OCT-1998;	98US-00167179.
PR	06-OCT-1998;	98US-0155266P.
PR	13-NOV-1998;	98US-00191838.
PR	13-NOV-1998;	98US-0155227P.
PR	03-DEC-1998;	98US-00205656.
XX		
PA	(INCY-) INCYTE PHARM INC.	
PI	Au-Young J, Lal P, Bandman O, Reddy R, Baughn MR, Yue H,	
PI	Hillman JL,	
XX		

DR MPI: 2000-317516/27.  
DR P-PsDB: AAY79510.  
XX  
XX Novel carboxylate-associated proteins used for the prevention and  
PT treatment of autoimmune/inflammatory disorders of e.g. the  
PT gastrointestinal and reproductive systems.  
PS  
PS Claim 9, Page 94, 104pp; English.  
XX  
XX The present sequence is that of cDNA coding for a novel human  
carboxylate-associated protein, termed CRBAP-6 (see AAY79510). The cDNA  
CC (Inveco clone 2821011) was initially identified in adenai tumour cDNA  
CC library ADRHUT06. CRBAP-6 has chemical and structural similarity with  
CC bovine lung surfactant protein D (32% identity). CRBAP-6 is expressed in  
CC the liver, kidney, ovary, gut, adrenal gland and secretory epithelium.  
CC The invention provides CRBAP-1 to -7 polynucleotides (see AAZ59491-48)  
CC and polypeptides (see AAY79505-11), as well as expression vectors, host  
CC cells, antibodies, agonists and antagonists. These are used in the  
CC diagnosis, treatment or prevention of disorders associated with CRBAP  
CC expression, especially autoimmune or inflammatory disorders,  
CC gastrointestinal disorders, infectious disorders, reproductive disorders,  
CC neurological disorders, eye disorders and cell proliferative disorders,  
CC including cancer. CRBAP polynucleotides are useful sources of probes and  
CC primers which can be used to detect CRBAP in a sample from a patient.  
XX They may also be administered as part of a gene therapy regime  
XX  
SQ Sequence 1253 BP; 287 A; 328 C; 400 G; 128 T; 0 U; 0 Other;

Query Match	100.0%	Score 1253;	DB 3;	Length 1253;
Best Local Similarity	100.0%	Pred. No. 2.1e-289;		
Matches 1253; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	GGGGGAGTGTCTCTCCGCGGGGACGAGGAGGAGGACGCGCGTTCGCGTTCGCGCGTCT	60
Db	1	GGGGGAGTGTCTCTCCGCGGGGACGAGGAGGAGGACGCGCGTTCGCGTTCGCGCGTCT	60
QY	61	CAGAGTGTGTGTCTCTGCGCTTCGAGATGAGGGGAACTTGCCCTCTGTGGGCGTTC	120
Db	61	CAGAGTGTGTGTCTCTGCGCGCTCAGGATGAGGGGAACTTGCCCTCTGTGGGCGTTC	120
QY	121	TAATCAGCCCTGGCGCTTCTGTCACTGCTGCACTTGACATCTCTGACGCGGCTGGCGATG	180
Db	121	TAATCAGCCCTGGCGCTTCTGTCACTGCTGCACTTGACATCTCTGACGCGGCTGGCGATG	180
QY	181	ACGCGTGTCTGTGCAGATCTCGTCCCTGGCGCTCAAAAGGGGATGCGGGAGAGAGGAG	240
Db	181	ACGCGTGTCTGTGCAGATCTCGTCCCTGGCGCTCAAAAGGGGATGCGGGAGAGAGGAG	240
QY	241	ACAAAGGCGCCCCCGGACGGCCTTGAAAGTGCGCCCAAGGAGAAAAAGAGACATGG	300
Db	241	ACAAAGGCGCCCCCGGACGGCCTTGAAAGTGCGCCCAAGGAGAAAAAGAGACATGG	300
QY	301	GGGACAAAGGACAGAAAGGCACTGTGGGTCGTCAATGAAAAATTGCTCCATTGGCTCTA	360
Db	301	GGGACAAAGGACAGAAAGGCACTGTGGGTCGTCAATGAAAAATTGCTCCATTGGCTCTA	360
QY	361	AAAGTGAAGAAAGAGATTTCCGGTGCATATAGACCCCGTGTCTTAATGAGAAACGAGGC	420
Db	361	AAAGTGAAGAAAGAGATTTCCGGTGCATATAGACCCCGTGTCTTAATGAGAAACGAGGC	420
QY	421	TCCCATGTATGTGCACGCCAGCTTGCGCAAGGCCATGCGGAGATGACAAACGAGTCTTC	480
Db	421	TCCCATGTATGTGCACGCCAGCTTGCGCAAGGCCATGCGGAGATGACAAACGAGTCTTC	480
QY	481	AGGTGACACGAGAGCTCAAGTTCAACAAGATGTGTGCGCGGTGCGGAGACGAGAG	540
Db	481	AGGTGACACGAGAGCTCAAGTTCAACAAGATGTGTGCGCGGTGCGGAGACGAGAG	540
QY	541	GCAAGATCTAAGTGTGTGTAAGAGAGAGAGCGCTACGCGAGCGCCAGCTGTCTGCGC	600
Db	541	GCAAGATCTAAGTGTGTGTAAGAGAGAGAGCGCTACGCGAGCGCCAGCTGTCTGCGC	600
QY	601	AGGCGCGCGGGGACGCTGAGCATGCCCCAAGACAGAGCTGCCAATGGCCTGATGGCG	660

[illegible]







Query Match	98.2%	Score 1230	DB 3	Length 1238
Beat Local Similarity	100.0%	Pred. No. 6.7e-284		
Matches 1230	Conservative 0	Mismatches 0	Indels 0	Gaps 0
<p>The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptor, TIR ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques</p>				
Sequence 1238 BP	293 A	321 C	389 G	235 T
0 U	0 Other			
24	GGGACGGGAGGAGCGCCCGTTGCGCTAGCGGCTGCTCAGAGATTGTTCTCCGTGCG	83		
1	GCGACGGGAGGAGCGCCCGTTGCGCTAGCGGCTGCTCAGAGATTGTTCTCCGTGCG	60		
84	CTCAGAGATGAGGGGAGATCTGGCCCTGTGTGGCGCTTCTATCAGCCTGGCTTCTCTGTC	143		
61	CTCAGAGATGAGGGGAGATCTGGCCCTGTGTGGCGCTTCTATCAGCCTGGCTTCTCTGTC	120		
144	CTGCTGCCATCTGGAACATCTTACGCCGCTGGCGATGACGCTGCTCTTGCAATCTCTC	203		
121	CTGCTGCCATCTGGAACATCTTACGCCGCTGGCGATGACGCTGCTCTTGCAATCTCTC	180		
204	GTCCCTGGCTCAAAAGGGGATGCGGGAGAGAGGAGCAAAAGGGGCCCGCGAGCGCT	263		
181	GTCCCTGGCTCAAAAGGGGATGCGGGAGAGAGGAGCAAAAGGGGCCCGCGAGCGCT	240		
264	GGAGAAGTCCGCCCGCAGCGGAGAAAAGAGACATCTGGGGACAAAGACAGAAAGGACGT	323		
241	GGAGAAGTCCGCCCGCAGCGGAGAAAAGAGACATCTGGGGACAAAGACAGAAAGGACGT	300		
334	GTGGGTCTGTCATGAAATAATGGTCCATTGGCTCTAAAGTTGAGAAAGAGATTCCGGT	383		
301	GTGGGTCTGTCATGAAATAATGGTCCATTGGCTCTAAAGTTGAGAAAGAGATTCCGGT	360		
384	GACATATGAGACCCCGTGTCTTATGAGAAACAGAGCTTCCCATGTGAGCGACGACGCTG	443		
361	GACATATGAGACCCCGTGTCTTATGAGAAACAGAGCTTCCCATGTGAGCGACGACGCTG	420		
444	GCGAAGCCATCGGGAGATGAGCAACAGGTCTCTCAGCTACACGACGACTCAAGTTC	503		
421	GCGAAGCCATCGGGAGATGAGCAACAGGTCTCTCAGCTACACGACGACTCAAGTTC	480		
504	ATCAAGATGCTGTGCGCGGTGTGCGGAGACGAGACGAGAAATCTTACTGTGTGTAAG	563		
481	ATCAAGATGCTGTGCGCGGTGTGCGGAGACGAGACGAGAAATCTTACTGTGTGTAAG	540		
564	GAGGAGAAAGCGCTTACGCGGACCGCCAGCTGTCTCTGACAGGCGCGGGGGCACGCTGAC	623		
541	GAGGAGAAAGCGCTTACGCGGACCGCCAGCTGTCTCTGACAGGCGCGGGGGCACGCTGAC	600		
624	ATGCCCAAGAGACGAGGCTGCTCAATGGCTGATGCGGACCTTACCTGGCGAAGCGGCTG	683		
601	ATGCCCAAGAGACGAGGCTGCTCAATGGCTGATGCGGACCTTACCTGGCGAAGCGGCTG	660		
684	GCCTGTCTTATCGGCATCAACGACCTTGAGAAAGAGAGGCGCTTCTGTATCTCTGAC	743		
661	GCCTGTCTTATCGGCATCAACGACCTTGAGAAAGAGAGGCGCTTCTGTATCTCTGAC	720		
744	CACCTCCCAATCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTACGAC	803		
721	CACCTCCCAATCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTACGAC	780		

QY	804	GAGGAGAGCTCCGTGAGAGATGTGTGGCTCTCGGCGCGCTGTGAACGACGTGGCTGTGCCACACC	863
Db	781	GAGAGAGAGCTCCGTGAGAGATGTGTGGCTCTCGGCGCGCTGTGAACGACGTGGCTGTGCCACACC	840
QY	864	ACCAATGTACTTCATGTGTGAGTTTGAACAAGGAGAACATGTGAGGCTCAGGCTGGGAGCTGC	923
Db	841	ACCAATGTACTTCATGTGTGAGTTTGAACAAGGAGAACATGTGAGGCTCAGGCTGGGAGCTGC	900
QY	924	CCATTGGGGGGCCCACATGTCTCCCTGCAGAGGTTGSCAGGGACAGAGCCCAACCAATGTGTGC	983
Db	901	CCATTGGGGGGCCCACATGTCTCCCTGCAGAGGTTGSCAGGGACAGAGCCCAACCAATGTGTGC	960
QY	964	CAGCCAGGAGAGCTGTCTCTCTGTGAAGGTTGGAAGCTTCACGAACTAAGAGGCTGTGTCTC	1043
Db	961	CAGCCAGGAGAGCTGTCTCTCTGTGAAGGTTGGAAGCTTCACGAACTAAGAGGCTGTGTCTC	1020
QY	1044	AAACTGAGAAATGTGGCCTTATGCTTAAGAGAGAAATGAAAGTGTCTCTGGGCTGTGTCTC	1103
Db	1021	AAACTGAGAAATGTGGCCTTATGCTTAAGAGAGAAATGAAAGTGTCTCTGGGCTGTGTCTC	1080
QY	1104	TGAAGAGACGAGATTTCATTAACCTGATTTGTAGCCCCCAATGCTATATGTAATTAATTAAC	1163
Db	1081	TGAAGAGACGAGATTTCATTAACCTGATTTGTAGCCCCCAATGCTATATGTAATTAATTAAC	1140
QY	1164	CAGAATTGCTCTTCCATTAAGCTTGTGCTTGTGCCAAGCTATACATTAATAATCTTTAAG	1223
Db	1141	CAGAATTGCTCTTCCATTAAGCTTGTGCTTGTGCCAAGCTATACATTAATAATCTTTAAG	1200
QY	1224	TAGTGCAGTAGTAAATCCAAAAAATAAATAA	1253
Db	1201	TAGTGCAGTAGTAAATCCAAAAAATAAATAA	1230
RESULT 4			
AAC58385			
ID	AAC58385	standard, cDNA, 1238 BP.	
AC	AAC58385;		
XX			
DT	29-JAN-2001	(first entry)	
XX			
DE	Human PRO1182	nucleotide sequence SEQ ID NO:50.	
XX			
KM	Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumorigenesis; identification; cancer; cytostatic; immunostimulant; antiangiogenic; leukæmia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blascoeolic disorder; inflammatory disorder; immunologic disorder; se.		
KM			
KW			
OS	Homo sapiens.		
XX			
PN	WO200053755-A2.		
XX			
PD	14-SEP-2000.		
XX			
PF	06-JAN-2000; 2000WO-US000376.		
XX			
PR	08-MAR-1999; 99WO-US005028.		
PR	08-JUN-1999; 99WO-US012252.		
PR	23-JUN-1999; 99US-0141037P.		
PR	07-JUL-1999; 99US-0143046P.		
PR	26-JUL-1999; 99US-0145698P.		
PR	30-NOV-1999; 99WO-US028313.		
PR	20-DEC-1999; 99WO-US030911.		
PR	05-JAN-2000; 2000WO-US000219.		
XX			
XX	(GETH ) GENENTECH INC.		
PI	Ashkenazi AJ Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;		



```

XX 02-JUN-1999; 99MO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145628P.
PR 28-JUL-1999; 99US-0146522P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99MO-US021090.
PR 15-SEP-1999; 99MO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99MO-US028313.
PR 01-DEC-1999; 99MO-US028301.
PR 16-DEC-1999; 99MO-US030095.
PR 20-DEC-1999; 99MO-US030911.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000376.
PR 11-FEB-2000; 2000MO-US003565.
PR 18-FEB-2000; 2000MO-US004341.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US004914.
PR 24-FEB-2000; 2000MO-US005004.
PR 02-MAR-2000; 2000MO-US005841.
PR 15-MAR-2000; 2000MO-US006884.
PR 20-MAR-2000; 2000MO-US007377.
XX
XX (GETH ) GENENTECH INC.
PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DJ;
PI Ferrara N, Fong S, Gerber H, Gertlesen ME, Goddard A,
PI Grimaldi CJ, Gurney AL, Kijavrin IJ, Napier MA, Pan U,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI: 2001-032160/04.
DR P-PSDB; AAB65261.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
XX
XX Claim 2; Fig 251; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
SQ
XX
XX Query Match 98.2%; Score 1230; DB 5; Length 1238;
XX Best Local Similarity 100.0%; Pred. No. 6; 7e-284;
XX Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 24 GCGAGGGGAGAGAGCGCCCGTTGCGCTAGCGCGTGCACAGAGTTGGTGTCTCGCTCGG 83
XX |||||
XX 1 GCGAGGGGAGAGAGCGCCCGTTGCGCTAGCGCGCTCAGAGATTGTGTCTCGCTCGG 60
XX |||||
XX CTCACGATGAGGGGGGAAATCTGGGCGGTGGGGGCTTATACAGCCCTGGGCTTCTGTCA 143
XX |||||
XX 61 CTCACGATGAGGGGGGAAATCTGGGCGGTGGGGGCTTATACAGCCCTGGGCTTCTGTCA 120
XX |||||
XX 144 CTGCTGCATCTGACATCTCTAGCGCGGTGGGGGATGAGCGCGTCTGTGACATCTCT 203

```

Db	121	CTGCTGCCATCTGGACATCTCAGCCGGCTGGCGATGACGGCTGCTGTGGAGATCTTC	180
Qy	204	GTCCCTGGCCTTCAAGGGGATGCGGAGAGAAAGGAGCAAAAGCGCCCCGGACGGCCT	263
Db	181	GTCCCTGGCCTCAAGGGGATGCGGAGAGAAAGGAGCAAAAGCGCCCCGGACGGCCT	240
Qy	264	GGAAAGTTCGGCCCCACGGGAGAAAAAGGACATGGGGGACAAAGACAAAGAGCACT	323
Db	241	GGAAAGTTCGGCCCCACGGGAGAAAAAGGACATGGGGGACAAAGACAAAGAGCACT	300
Qy	324	GGGGTGGTATGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGT	383
Db	301	GGGGTGGTATGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGT	360
Qy	384	GACATAGGACCCCTGTGTCTTAATGAGAACAGGCGCTCCATGTGAGTGCAGCCACTG	443
Db	361	GACATAGGACCCCTGTGTCTTAATGAGAACAGGCGCTCCATGTGAGTGCAGCCACTG	420
Qy	444	CGCAAGGCCATCGGGGAGATGGACAAACAGGTCTCTCAGCTGACCAAGCACTCAAGTTC	503
Db	421	CGCAAGGCCATCGGGGAGATGGACAAACAGGTCTCTCAGCTGACCAAGCACTCAAGTTC	480
Qy	504	ATCAAGATTCGTGTGCGCGGTGTGGCGGACGAGAGAGCAATCTACCTGTGTGGAG	563
Db	481	ATCAAGATTCGTGTGCGCGGTGTGGCGGACGAGAGAGCAATCTACCTGTGTGGAG	540
Qy	564	GAGAGAAAGCGTATGCGGACGCGCAGCTGTCTTCACAGGGCGCGGGGGCAACGTGAGC	623
Db	541	GAGAGAAAGCGTATGCGGACGCGCAGCTGTCTTCACAGGGCGCGGGGGCAACGTGAGC	600
Qy	624	ATGCCAAGACGAGGCTGCCAATGGCTGATGCGCGCATACCTGTGGCGGAAGCGGCTTG	683
Db	601	ATGCCAAGACGAGGCTGCCAATGGCTGATGCGCGCATACCTGTGGCGGAAGCGGCTTG	660
Qy	684	GCCCGTGTCTTCAATGGCATCAACGACCTGAGAAAGAGGGGCGCTTCGTGTATCTTGAC	743
Db	661	GCCCGTGTCTTCAATGGCATCAACGACCTGAGAAAGAGGGGCGCTTCGTGTATCTTGAC	720
Qy	744	CACCTCCCATGCGGACCTTCAACAAAGTGGCGCAGGGGAGACCCCAAAATGCGTACGAC	803
Db	721	CACCTCCCATGCGGACCTTCAACAAAGTGGCGCAGGGGAGACCCCAAAATGCGTACGAC	780
Qy	804	GAGGAGACCTGGCGGAGATGGTGGCCTTCGGCGCGCTGAAACGACGTGGCTTGCCACAC	863
Db	781	GAGGAGACCTGGCGGAGATGGTGGCCTTCGGCGCGCTGAAACGACGTGGCTTGCCACAC	840
Qy	864	ACCATGTACTCATGTGTGAGTTTGAACAAAGAAACATGTGACCTCAGGCTGGGGCTGC	923
Db	841	ACCATGTACTCATGTGTGAGTTTGAACAAAGAAACATGTGACCTCAGGCTGGGGCTGC	900
Qy	924	CCATTGGGGGGCCCAATGTCCTCCGACAGGTTGGAGAGGACAGAGCCCAACATGGTGC	983
Db	901	CCATTGGGGGGCCCAATGTCCTCCGACAGGTTGGAGAGGACAGAGCCCAACATGGTGC	960
Qy	984	CAGCCAGGAGGTGTCCCTCTGTGAAGGGTGAAGGCTCACTAGTATGAGGGCTGTGTCT	1044
Db	961	CAGCCAGGAGGTGTCCCTCTGTGTGAAGGGTGAAGGCTCACTAGTATGAGGGCTGTGTCT	1022
Qy	1044	AAACTGAGAAAATGGCCTTATGCTTAAAGAGAAAATGAAGTGTCTCTGGGGTGTGTCTC	1104
Db	1021	AAACTGAGAAAATGGCCTTATGCTTAAAGAGAAAATGAAGTGTCTCTGGGGTGTGTCTC	1082
Qy	1104	TGAAGAACAGAGTTTCAATACGCTATTTGTGCCCCCAATGTCATTAATTAATTTATAC	1164
Db	1081	TGAAGAACAGAGTTTCAATACGCTATTTGTGCCCCCAATGTCATTAATTAATTTATAC	1144
Qy	1164	CAGATTGTCTCTTCATTAAGCTTGTGCTTGTCCAAAGCTATACATTAATCTTTAAG	1224
Db	1141	CAGATTGTCTCTTCATTAAGCTTGTGCTTGTCCAAAGCTATACATTAATCTTTAAG	1202
Qy	1224	TAGTGCAGTATTAAATCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1284

DB 1201 TAGTCAGTAGTTAAGTCCAAAAA 1230

RESULT 6

ABL88155

AC ABL88155;

16-MAY-2002 (first entry)

Human PRO1182 cDNA sequence SEQ ID NO:167.

Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
age-related macular degeneration; arterial restenosis; angina;  
rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
wound healing; chromosome mapping; gene mapping; gene; ss.

Homo sapiens.

WO200200690-A2.

03-JAN-2002.

20-JUN-2001; 2001WO-US019692.

23-JUN-2000; 2000US-0213637P.

20-JUL-2000; 2000US-0219556P.

25-JUL-2000; 2000US-0220624P.

28-JUL-2000; 2000WO-US020710.

02-AUG-2000; 2000US-0226959P.

17-AUG-2000; 2000US-00643657.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000WO-US023328.

07-SEP-2000; 2000US-0230978P.

18-SEP-2000; 2000US-0064610.

24-OCT-2000; 2000US-00665350.

08-NOV-2000; 2000US-00709238.

08-NOV-2000; 2000WO-US030952.

10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

22-JAN-2001; 2001US-00767609.

28-FEB-2001; 2001US-00796498.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006520.

09-MAR-2001; 2001US-00802706.

14-MAR-2001; 2001US-00808689.

22-MAR-2001; 2001US-00816744.

05-APR-2001; 2001US-00828366.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001US-0086028.

25-MAY-2001; 2001WO-US017092.

30-MAY-2001; 2001US-00870574.

01-JUN-2001; 2001WO-US017443.

01-JUN-2001; 2001WO-US017800.

(GERTH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A, Godowski PJ, Guirney AL, Hillan KU, Martens SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,

WPI; 2002-090516/12.

DR P-PSDB; ABB84900.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

Claim 2; Fig 167; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytosolic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention

Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Query Match 98.2%; Score 1230; DB 6; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 6; 7e-284;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 GCGACGGGCGAGAGCGCCGCTTGCCTAGCGCTGCTAGAGTGTGCTGCTGCG 83

1 GCGACGGGCGAGAGCGCCGCTTGCCTAGCGCTGCTAGAGTGTGCTGCTGCG 60

84 CTGAGATAGAGGGGGAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 143

61 CTGAGATAGAGGGGGAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 120

144 CTGCTGCATCTGAGATCTGAGCGCGCTGAGGAGTGAAGCGCTGCTGCTGCTGCTC 203

121 CTGCTGCATCTGAGATCTGAGCGCGCTGAGGAGTGAAGCGCTGCTGCTGCTGCTC 180

204 GTCCCTGCTGCTGAGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTC 263

181 GTCCCTGCTGCTGAGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTC 240

264 GGAAGAGTGGCGCCCGAGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTC 323

241 GGAAGAGTGGCGCCCGAGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTC 300

324 GTGGGTCTGCTGAGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTC 383

301 GTGGGTCTGCTGAGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTC 360

384 GACATGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 443

361 GACATGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

444 CGAAGGCGCATGCGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTGCTG 503

421 CGAAGGCGCATGCGGAGTGAAGCGCGCTGAGGAGTGAAGCGCGCTGCTGCTGCTGCTG 480

504 ATCAAGATGCTGCTGCGCGTGTGCGGAGCGAGAGCAAGATCTGCTGCTGCTGCTGCTG 563

481 ATCAAGATGCTGCTGCGCGTGTGCGGAGCGAGAGCAAGATCTGCTGCTGCTGCTGCTG 540

564 GAGAGAGAGCGCTGAGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623

541 GAGAGAGAGCGCTGAGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

624 ATGCCCAAGAGAGCGCTGAGCGGAGCGCGCTGAGCGGAGCGCGCTGCTGCTGCTGCTGCTG 683

601 ATGCCCAAGAGAGCGCTGAGCGGAGCGCGCTGAGCGGAGCGCGCTGCTGCTGCTGCTGCTG 660

```

QY 684 GCCGTGTCCTCATCGGATCAAGACCTGGAGAGAGGGGCGCTTGCTGTAAGTCTAC 743
Db 661 GCGGTGTCCTCATCGGATCAAGACCTGGAGAGAGGGGCGCTTGCTGTAAGTCTAC 720
QY 744 CACTCCCCCATGCGGACCTTCAACAAGTGGCGACGCGTGAGCCCAACATGCTTACAC 803
Db 721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGACGCGTGAGCCCAACATGCTTACAC 780
QY 804 GAGAGAGACTGCTGTGAGATGTGTGCTGCGGCGGCTGGAACAGATGCTGCTGACAC 863
Db 781 GAGAGAGACTGCTGTGAGATGTGTGCTGCGGCGGCTGGAACAGATGCTGCTGACAC 840
QY 864 ACCATGTAATTCATGTGTGAGTGTGACAAAGAGAAATCATGTGAGCTCAAGGCTGGGCTGC 923
Db 841 ACCATGTAATTCATGTGTGAGTGTGACAAAGAGAAATCATGTGAGCTCAAGGCTGGGCTGC 900
QY 924 CCATTGGGGGGCCCCACATGTCCTGCGAGGTTGGCGAGGACAGAGCCCAACATGCTGC 983
Db 901 CCATTGGGGGGCCCCACATGTCCTGCGAGGTTGGCGAGGACAGAGCCCAACATGCTGC 960
QY 984 CAGCCAGGAGCTGTCTCTGTGAAAGGTGAGGCTCACTGATGAGGGCTGTTGCT 1043
Db 961 CAGCCAGGAGCTGTCTCTGTGAAAGGTGAGGCTCACTGATGAGGGCTGTTGCT 1020
QY 1044 AAACAGAGAAATGGCTATGCTTAAGAGAAATGAAGTTCCTGGGGCTGCTC 1103
Db 1021 AAACAGAGAAATGGCTATGCTTAAGAGAAATGAAGTTCCTGGGGCTGCTC 1080
QY 1104 TGAAGAGACAGAGTTTCAATTAAGTATGTAAGCCCAATGCTATTAATTAATTAAC 1163
Db 1081 TGAAGAGACAGAGTTTCAATTAAGTATGTAAGCCCAATGCTATTAATTAATTAAC 1140
QY 1164 CAGAAATGCTCTTCCATTAAGTGTGCTTGTCCAAAGCTATACATTAATTAATTAAG 1223
Db 1141 CAGAAATGCTCTTCCATTAAGTGTGCTTGTCCAAAGCTATACATTAATTAATTAAG 1200
QY 1224 TAGTGAGTAGTAAAGTCCAAAAA 1253
Db 1201 TAGTGAGTAGTAAAGTCCAAAAA 1230

RESULT 7
ABL95644
ID ABL95644 standard; cDNA; 1238 BP.
XX
AC ABL95644;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA P101182 SEQ ID NO: 167.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnery;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PP 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

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PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00766498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX
DR WPI, 2002-171999/122.
DR P-P8DB; ABB95506.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 167; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial revascularisation, rheumatoid arthritis,
CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
XX
Query Match 98.2%; Score 1230; DB 6; Length 1238;
Best Local Similarity 100.0%; Pred. No. 6.7e-284;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 GCGACGGCAGAGAGCCCGCTTCCGCTAGCGCGGCTCAGAGAGTGTGCTGCTGCG 83

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DB 1 GGGAGGGGAGGACGCGCCCGTTGCGCTAGCGCGTCTCAGAGGTTGGTGTCTGCTGCTCG 60  
QY 84 CTCAGAGTGAAGGGGAAATTTGGCCCTGGTGGCGTTCTTAATCAGCTTGCCCTTCTGCA 143  
DB 61 CTCAGAGTGAAGGGGAAATTTGGCCCTGGTGGCGTTCTTAATCAGCTTGCCCTTCTGCA 120  
QY 144 CTGCTGCCATCTGGAATCTCAGCGCGGCTGGCGATGACGCTGTCTGTGAGATCTCTC 203  
DB 121 CTGCTGCCATCTGGAATCTCAGCGCGGCTGGCGATGACGCTGTCTGTGAGATCTCTC 180  
QY 204 GTCCCTGGCTTCAAAAGGGATGCGGAGAGAAAGGAGACAAAGCGCCCGCGACGCGCT 263  
DB 181 GTCCCTGGCTTCAAAAGGGATGCGGAGAGAAAGGAGACAAAGCGCCCGCGACGCGCT 240  
QY 264 GGAAGAGTCCGCGCCCAAGGAGAGAAAGGAGACATGGGAGCAAAAGGAGGAGCT 323  
DB 241 GGAAGAGTCCGCGCCCAAGGAGAGAAAGGAGACATGGGAGCAAAAGGAGGAGCT 300  
QY 324 GTGGGTGCTCATGAGAAATTTGGTCCCATTTGGCTCTAAAGGTTGAGAAAGGATTTCCGGT 383  
DB 301 GTGGGTGCTCATGAGAAATTTGGTCCCATTTGGCTCTAAAGGTTGAGAAAGGATTTCCGGT 360  
QY 384 GACATAGAGACCCCTGTGTCTTAATGAGAACCGGCTCCCATGTGATGAGCCAGCTG 443  
DB 361 GACATAGAGACCCCTGTGTCTTAATGAGAACCGGCTCCCATGTGATGAGCCAGCTG 420  
QY 444 GCGAAGGCTATCGGGAGATGAGCAACAGGTTCTTCAAGCTGACCAAGGAGCTCAAGTTC 503  
DB 421 GCGAAGGCTATCGGGAGATGAGCAACAGGTTCTTCAAGCTGACCAAGGAGCTCAAGTTC 480  
QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGACGAGAGCAAGATCTACTCTGTGTAAG 563  
DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGCGAGACGAGAGCAAGATCTACTCTGTGTAAG 540  
QY 564 GAGAGAGAGCGCTACGCGGACGCGCAAGCTGTCTGCGAGGCGCGGGGAGCAAGCTGAGC 623  
DB 541 GAGAGAGAGCGCTACGCGGACGCGCAAGCTGTCTGCGAGGCGCGGGGAGCAAGCTGAGC 600  
QY 624 ATGCCCAAGAGAGAGGCTGCAATGAGCTGATGAGCGGCTGATGAGCGGAGCGGAGCTG 683  
DB 601 ATGCCCAAGAGAGAGGCTGCAATGAGCTGATGAGCGGCTGATGAGCGGAGCGGAGCTG 660  
QY 684 GCCCGTGTCTTCAATCGGATCAACGACCTGAGAGAGAGGAGGCGGCTTGTGTACTCTGAC 743  
DB 661 GCCCGTGTCTTCAATCGGATCAACGACCTGAGAGAGAGGAGGCGGCTTGTGTACTCTGAC 720  
QY 744 CACTCCCCCAGCGGACCTTAAACAATGAGCGGAGCGGCTGAGCCCAATGCTTACGAC 803  
DB 721 CACTCCCCCAGCGGACCTTAAACAATGAGCGGAGCGGCTGAGCCCAATGCTTACGAC 780  
QY 804 GAGAGAGAGCTGCTGAGATGATGAGCTGCGGCGGCTGAGAACGAGTGGCTGACCAAC 863  
DB 781 GAGAGAGAGCTGCTGAGATGATGAGCTGCGGCGGCTGAGAACGAGTGGCTGACCAAC 840  
QY 864 ACATATGATCTTCAATGAGTGAATTTGACAGAGAAATGTGAGCTCAGGCTGGGAGCTGC 923  
DB 841 ACATATGATCTTCAATGAGTGAATTTGACAGAGAAATGTGAGCTCAGGCTGGGAGCTGC 900  
QY 924 CCATTTGGGGGCGCCCAATGTCCTGCAAGGTTGGCAGAGGAGCAAGGCCCAACATGCTGC 983  
DB 901 CCATTTGGGGGCGCCCAATGTCCTGCAAGGTTGGCAGAGGAGCAAGGCCCAACATGCTGC 960  
QY 984 CAGCAGAGAGCTGCTGCTGTAAGAGGTTGAGAGCTCACTGATGAGAGGAGCTGTTGCT 1043  
DB 961 CAGCAGAGAGCTGCTGCTGTAAGAGGTTGAGAGCTCACTGATGAGAGGAGCTGTTGCT 1020  
QY 1044 AAAATGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTGTCTCTGGGCTGCTGCTC 1103  
DB 1021 AAAATGAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTGTCTCTGGGCTGCTGCTC 1080  
QY 1104 TGAAGAGCAGAGTTTCAATACCTGTATGTAGGCCCAATGTATTAATTAATTTACC 1163

DB 1081 TGAAGAGCAGAGTTTCAATACCTGTATGTAGGCCCAATGTATTAATTAATTTACC 1140  
QY 1164 CAGAAATGCTCTTCCATTAAGGCTTGTGCTTGTCCAAAGCTATACATAAATCTTTAG 1223  
DB 1141 CAGAAATGCTCTTCCATTAAGGCTTGTGCTTGTCCAAAGCTATACATAAATCTTTAG 1200  
QY 1224 TAGTCAGTAGTTAAGTCCCAAAAAA 1253  
DB 1201 TAGTCAGTAGTTAAGTCCCAAAAAA 1230  
RESULT 8  
ID ACA64399 standard, cDNA, 1238 BP.  
XX ACA64399;  
XX 17-JUN-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO1182 cDNA.  
XX Human, secreted and transmembrane protein; cytosolic; anti-HIV;  
XX virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;  
XX PEO; pharmaceutical; diagnostic; biosensor; bioindicator; malignancy;  
XX cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;  
XX lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;  
XX drug screening; gene; ss.  
XX Homo sapiens.  
XX OS  
XX US2003003531-A1.  
XX PN  
XX PD 02-JAN-2003.  
XX  
XX 19-NOV-2001; 2001US-00989734.  
XX PF  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WC-US020069.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 24-NOV-1997; 97US-0066770P.  
XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0078910P.  
XX 28-APR-1998; 98US-0083322P.  
XX 07-MAY-1998; 98US-0084600P.  
XX 28-MAY-1998; 98US-0087106P.  
XX 02-JUN-1998; 98US-0087607P.  
XX 02-JUN-1998; 98US-0087609P.  
XX 02-JUN-1998; 98US-0087759P.  
XX 03-JUN-1998; 98US-0087827P.  
XX 04-JUN-1998; 98US-0088021P.  
XX 04-JUN-1998; 98US-0088025P.  
XX 04-JUN-1998; 98US-0088026P.  
XX 04-JUN-1998; 98US-0088028P.  
XX 04-JUN-1998; 98US-0088029P.  
XX 04-JUN-1998; 98US-0088030P.  
XX 04-JUN-1998; 98US-0088033P.  
XX 04-JUN-1998; 98US-0088326P.  
XX 05-JUN-1998; 98US-0088167P.  
XX 05-JUN-1998; 98US-0088202P.  
XX 05-JUN-1998; 98US-0088212P.  
XX 05-JUN-1998; 98US-0088217P.  
XX 09-JUN-1998; 98US-0088655P.  
XX 10-JUN-1998; 98US-0088734P.  
XX 10-JUN-1998; 98US-0088738P.  
XX 10-JUN-1998; 98US-0088742P.  
XX 10-JUN-1998; 98US-0088810P.  
XX 10-JUN-1998; 98US-0088824P.  
XX 10-JUN-1998; 98US-0088826P.  
XX 11-JUN-1998; 98US-0088858P.  
XX 11-JUN-1998; 98US-0088861P.  
XX 11-JUN-1998; 98US-0088876P.

PR	12-JUN-1998;	98US--0089105P.
PR	16-JUN-1998;	98US--0089446P.
PR	16-JUN-1998;	98US--0089511P.
PR	16-JUN-1998;	98US--0089514P.
PR	17-JUN-1998;	98US--0089532P.
PR	17-JUN-1998;	98US--0089538P.
PR	17-JUN-1998;	98US--0089559P.
PR	17-JUN-1998;	98US--0089592P.
PR	17-JUN-1998;	98US--0089600P.
PR	17-JUN-1998;	98US--0089653P.
PR	18-JUN-1998;	98US--0089801P.
PR	18-JUN-1998;	98US--0089907P.
PR	18-JUN-1998;	98US--0089908P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98WO-US019437.
PR	07-OCT-1998;	98WO-US021141.
PR	01-DEC-1998;	98WO-US025108.
PR	05-JAN-1999;	99WO-US000106.
PR	08-MAR-1999;	99WO-US005028.
PR	02-JUN-1999;	99WO-US012822.
PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028301.
PR	01-DEC-1999;	99WO-US028634.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003585.
PR	18-FEB-2000;	2000WO-US004341.
PR	22-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	30-MAR-2000;	2000WO-US008439.
PR	15-MAY-2000;	2000WO-US013358.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US015941.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	11-AUG-2000;	2000WO-US022031.
PR	23-AUG-2000;	2000WO-US023522.
PR	24-AUG-2000;	2000WO-US023528.
PR	08-NOV-2000;	2000WO-US030952.
PR	01-DEC-2000;	2000WO-US032678.
PR	28-FEB-2001;	2001WO-US006520.
PR	01-JUN-2001;	2001WO-US017800.
PR	20-JUN-2001;	2001WO-US019682.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.
PR	28-AUG-2001;	2001US--00941992.
XX		
PA	(GETH ) GENENTECH INC.	
XX		
P1	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,	
P1	Ferrara N, Fong S, Gebler H, Gerritsen ME, Goddard A, Godowski P,	
P1	Grimaldi JC, Gunney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,	
P1	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,	
P1	Zhang Z,	
XX		
DR	WPI; 2003-352829/33.	
DR	P-PeDB; ABU72552.	
XX		
PT	New genes and secreted and transmembrane polypeptides (e.g. PRO183 or	
PT	PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's	
PT	sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's	
XX	disease.	

PS Claim 1, Fig 251; 663bp; English.

XX The invention describes a new isolated nucleic acid molecule comprising  
CC the full length coding sequence of the DNA deposited with the American  
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-P7A, 819-P7A,  
CC 209439, 203135, etc.) or a sequence with at least 80% identity to a DNA  
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
CC are particularly useful for detecting or treating e.g. malignancies or  
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,  
CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
CC disease in mammals. The PRO polypeptides are useful in drug screening,  
CC particularly as targets for therapeutic intervention in these diseases,  
CC and in the diagnostic determination of the presence of these diseases.  
CC The PRO polypeptides are also useful as molecular weight markers, or for  
CC chromosome identification. The PRO genes are useful as hybridisation  
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
CC The PRO genes may also be used in gene therapy, particularly for  
CC replacing a defective gene. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide

XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Query Match 98.2%; Score 1230; DB 8; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 6.7e-264;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 24 GCGAGCGGGCAGAGACGCCCGTTCGCGCTACGCGCTCTCAGAGAGTGTGTCTCGCTCGG 83  
DB 1 GCGAGCGGGCAGAGACGCCCGTTCGCGCTACGCGCTCTCAGAGAGTGTGTCTCGCTCGG 60

QY 84 CTCAGAGTAGGGGGAAATCTGGCCCTGGTGGCGCTTCTAATCAGCCTTGCTCTGTCTCA 143  
DB 61 CTCAGAGTAGGGGGAAATCTGGCCCTGGTGGCGCTTCTAATCAGCCTTGCTCTGTCTCA 120

QY 144 CTGCTGCGCATCTGGACATCTCTCAGCGCGCTGGCCATACGCTGCTCTGTGCAATCTCTC 203  
DB 121 CTGCTGCGCATCTGGACATCTCTCAGCGCGCTGGCCATACGCTGCTCTGTGCAATCTCTC 180

QY 204 GTCCCTGGCCTCAAAAGGGGATGCGGGAGAGAAAGGGAGCAAAAGGGCGCCCGAGCGACT 263  
DB 181 GTCCCTGGCCTCAAAAGGGGATGCGGGAGAGAAAGGGAGCAAAAGGGCGCCCGAGCGACT 240

QY 264 GGAAGAGTCTGGCGCCCGCAGGAGAAAGAGAGCATGGGGAGCAAAAGAGCAGAAAGCGACT 323  
DB 241 GGAAGAGTCTGGCGCCCGCAGGAGAAAGAGAGCATGGGGAGCAAAAGAGCAGAAAGCGACT 300

QY 324 GTGGTCTGTCAATGAAAAATTGCTCCATTGGCTCTAAAGGTGAGAAAGAGATTCCGCT 383  
DB 301 GTGGTCTGTCAATGAAAAATTGCTCCATTGGCTCTAAAGGTGAGAAAGAGATTCCGCT 360

QY 384 GACATAGGACCCCGTGTCTTAATGGAACAACAGGCCCTCCATGTAATGACGACGCAAGCTG 443  
DB 361 GACATAGGACCCCGTGTCTTAATGGAACAACAGGCCCTCCATGTAATGACGACGCAAGCTG 420

QY 444 CGCAAGGCGCATCGGGGAGATGAGACACAGAGCTCTCAGCTGACCAAGAGCTCAAGTTTC 503  
DB 421 CGCAAGGCGCATCGGGGAGATGAGACACAGAGCTCTCAGCTGACCAAGAGCTCAAGTTTC 480

QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGAGAGACCAAGATCTACCTGTGTGTAAG 563  
DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGGAGACGAGAGACCAAGATCTACCTGTGTGTAAG 540

QY 564 GAGAGAAAGCGCTACGCGAGAGCCCAAGCTGTCTTCGACAGGGCCGCGGGGGACAGCTGAGC 623  
DB 541 GAGAGAAAGCGCTACGCGAGAGCCCAAGCTGTCTTCGACAGGGCCGCGGGGGACAGCTGAGC 600

QY 624 ATGCCCAAGAGCAGAGGCTGCCAATGGCTGTAATGGCGGATACCTGAGCGCAAGCGGCGCTG 683  
DB 601 ATGCCCAAGAGCAGAGGCTGCCAATGGCTGTAATGGCGGATACCTGAGCGCAAGCGGCGCTG 660

QY 684 GCCCGTGTCTTATCGGCATACACGACCTTGAGAGAGAGGGCGCCTTGTGTATCTCTGAC 743



DB 661 GCCCGTCTTCATCGGCATCAACGACTGAGAAAGAGGGCGCTTCGTACTGTGAC 720  
QY 744 CACTCCCCCATGGGACCTTCAACAAGTGGCCAGCGGTGACCCCAACATGCTTACGAC 803  
DB 721 CACTCCCCCATGGGACCTTCAACAAGTGGCCAGCGGTGACCCCAACATGCTTACGAC 780  
QY 804 GAGAGAGACTGCGTGGAGATGGTGGCTTCGGCGGCTGGAGACGATGCGCTGACACAC 863  
DB 781 GAGAGAGACTGCGTGGAGATGGTGGCTTCGGCGGCTGGAGACGATGCGCTGACACAC 840  
QY 864 ACCATGTCCTTATGTGTGAGATTGACAAAGAGAAATGTGAGCTCAGGCTGGGCTGAC 923  
DB 841 ACCATGTCCTTATGTGTGAGATTGACAAAGAGAAATGTGAGCTCAGGCTGGGCTGAC 900  
QY 924 CCATTGGGGGCCCAATGTCCTCAGGGTGGAGGAGACAGAGCCCAACATGATGAC 983  
DB 901 CCATTGGGGGCCCAATGTCCTCAGGGTGGAGGAGACAGAGCCCAACATGATGAC 960  
QY 984 CAGCCAGGAGCTGTCTCTGTGAGAGGCTGAGAGGCTCACTGATGAGAGGCTGTGCT 1043  
DB 961 CAGCCAGGAGCTGTCTCTGTGAGAGGCTGAGAGGCTCACTGATGAGAGGCTGTGCT 1020  
QY 1044 AAACGAGAGAAATGGCTATGCTTAAAGAGAAATGAAGTTCCTGGGCTGCTGCTC 1103  
DB 1021 AAACGAGAGAAATGGCTATGCTTAAAGAGAAATGAAGTTCCTGGGCTGCTGCTC 1080  
QY 1104 TGAAGACAGAGTTCATTAAGCTGATTTAGAGCCCAATGCTATGATTAATTAAC 1163  
DB 1081 TGAAGACAGAGTTCATTAAGCTGATTTAGAGCCCAATGCTATGATTAATTAAC 1140  
QY 1164 CAGAAATGCTCTTCAATTAAGCTTGTGCTTGCATTAACATTAATTAATTTAAG 1223  
DB 1141 CAGAAATGCTCTTCAATTAAGCTTGTGCTTGCATTAACATTAATTAATTTAAG 1200  
QY 1224 TAGTCAGTAAAGTCAAAAAA 1253  
DB 1201 TAGTCAGTAAAGTCAAAAAA 1230

RESULT 9  
ABX80858  
ID ABX80858 standard; cDNA, 1238 BP.  
XX AC ABX80858;  
XX DT 22-APR-2003 (first entry)  
XX DE Human secreted/transmembrane protein cDNA, #144.  
XX KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;  
KW tumour-associated antigenic target; TAT; ADPBT;  
XX antibody-dependent enzyme mediated produg therapy; cytosolic.  
OS Homo sapiens.  
XX PN US2003027162-A1.  
XX PD 06-FEB-2003.  
XX PF 15-NOV-2001; 2001US-00997428.  
XX PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-006250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.  
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PR 02-JUL-1998; 98US-0091646P.



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 PR 10-JUL-1998; 98US-0092182P.  
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 PR 08-MAR-1999; 98US-01005028.  
 PR 12-MAR-1999; 98US-0123957P.  
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 PR 23-JUN-1999; 98US-0143048P.  
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 PR 26-JUL-1999; 98US-0144698P.  
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 PR 17-AUG-1999; 98US-0149396P.  
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PR 05-JAN-2000; 2000US-0000219.  
 PR 06-JAN-2000; 2000US-0000376.  
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 PR 18-FEB-2000; 2000US-0000431P.  
 PR 22-FEB-2000; 2000US-00004414.  
 PR 24-FEB-2000; 2000US-00004914.  
 PR 02-MAR-2000; 2000US-00005004.  
 PR 10-MAR-2000; 2000US-00005841.  
 PR 15-MAR-2000; 2000US-00006319.  
 PR 15-MAR-2000; 2000US-00006884.  
 PR 30-MAR-2000; 2000US-00007377.  
 PR 30-MAR-2000; 2000US-00008439.  
 PR 17-MAY-2000; 2000US-00013705.  
 PR 22-MAY-2000; 2000US-00014042.  
 PR 30-MAY-2000; 2000US-00014941.  
 PR 02-JUN-2000; 2000US-00015264.  
 PR 23-JUN-2000; 2000US-0213637P.  
 PR 28-JUL-2000; 2000US-02020710.  
 PR 11-AUG-2000; 2000US-02022031.  
 PR 23-AUG-2000; 2000US-02023522.  
 PR 24-AUG-2000; 2000US-02023328.

Query Match 98.2%; Score 1230; DB 8; Length 1238;  
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 DB 1 GCGACGGGACGAGCGCCCGTTGCGCTAGCGCGTGTGCTGAGAGTTGTGCTGCTGCG 60

QY 84 CTCAGAGTGGAGGGGAACTGCGCCCTGTGCGCCCTTCAATCAGCTGGCCCTTCTGCA 143  
 DB 61 CTCAGAGTGGAGGGGAACTGCGCCCTGTGCGCCCTTCAATCAGCTGGCCCTTCTGCA 120

QY 144 CTGCTGCCATCTGACATCTCTCAGCCGCTGCGATGACGCTGCTGTGCAATCTCTC 203  
 DB 121 CTGCTGCCATCTGACATCTCTCAGCCGCTGCGATGACGCTGCTGTGCAATCTCTC 180

QY 204 GTCCCTGGCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
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QY 224 GGAAGAGTGGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
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QY 324 GTGGGTGCTCATGTGAGAAATTTGCTCCATTTGCTTAAAGGTGAGAAAGATTCGGT 383  
 DB 301 GTGGGTGCTCATGTGAGAAATTTGCTCCATTTGCTTAAAGGTGAGAAAGATTCGGT 360

QY 384 GACATGAGAGCCCGCTGTGCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443  
 DB 361 GACATGAGAGCCCGCTGTGCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

QY 444 CGCAAGGCTATCGGAGAGATGAGACCAAGTCTTCAAGCTGACCAAGGAGCTCAAGTTC 503  
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QY 504 ATCAAGAAATGCTGTGCGCGGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
 DB 481 ATCAAGAAATGCTGTGCGCGGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 544 GAGAGAAAGCGCTACGCGAGAGCGCCAGCTGTCTGCGAGAGAGAGAGAGAGAGAGAG 623  
 DB 541 GAGAGAAAGCGCTACGCGAGAGCGCCAGCTGTCTGCGAGAGAGAGAGAGAGAGAGAG 600

QY 624 ATGCCCAAGAGAGAGAGCTGCGCAATGAGCTTATGAGCTGAGATCTGCGGAGAGAGAG 683  
 DB 601 ATGCCCAAGAGAGAGAGCTGCGCAATGAGCTTATGAGCTGAGATCTGCGGAGAGAGAG 660

QY 684 GCCCGTGTCTTCAATGAG 743

Dh 661 GCCCGTGTCTTCATCGGCATCAAGACCTGAGGAAGAGGGGCGCTTGCTACTCTAC 720  
Qy 744 CACTCCCCCATGCGGACCTTCAACAAGTGGCCGACGGTGAGCCCAACAATGCTTAGAC 803  
Db 721 CACTCCCCCATGCGGACCTTCAACAAGTGGCCGACGGTGAGCCCAACAATGCTTAGAC 780  
Qy 804 GAGGAGACTGCGTGGAGATGGTGGCTCGGGCGGCTGGAACGACTGGCCGACAGC 863  
Db 781 GAGGAGACTGCGTGGAGATGGTGGCTCGGGCGGCTGGAACGACTGGCCGACAGC 840  
Qy 864 ACCATGTACTTATGTGAGTTTGAACAAGAAACATGTAGCCTCAGGCTGGGGCTGC 923  
Db 841 ACCATGTACTTATGTGAGTTTGAACAAGAAACATGTAGCCTCAGGCTGGGGCTGC 900  
Qy 924 CCATTGGGGGGCCCAATGTCCTCGCAGGGTTGGAGGGAACAGAGCCCAACATGTGTC 983  
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Db 1201 TAGTGCAGTACTTAAGTCCAAAAA 1230

RESULT 10  
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ID ACD44367 standard; cDNA; 1238 BP.  
XX ACD44367;  
AC ACD44367;  
DT 10-SBP-2003 (first entry)  
XX  
DE cDNA encoding human PRO1182 polypeptide.  
KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
KW gene therapy; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2002127576-A1.  
XX  
XX 12-SBP-2002.  
XX  
XX 14-NOV-2001; 2001US-00991073.  
XX  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WO-US020069.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
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XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0078910P.  
XX 28-APR-1998; 98US-0083322P.  
XX 07-MAY-1998; 98US-0084600P.  
XX 28-MAY-1998; 98US-0087106P.  
XX 02-JUN-1998; 98US-0087607P.

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PR 04-JUN-1998; 98US-0088021P.  
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PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
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PR 18-JUN-1998; 98US-0089807P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 18-JUN-1998; 98US-0091930P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 10-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 28-JUN-2000; 2000WO-US015264.  
PR 11-AUG-2000; 2000WO-US020710.  
PR 23-AUG-2000; 2000WO-US022031.  
PR 24-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GENENTECH INC.  
XX Aekhenazi AJ, Baker KP, Botstein D, Desnoyers J, Eaton DR,  
XX Ferrara N, Fong S, Gether H, Gerlitsen MB, Goddard A, Godowski PJ,  
XX Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Pooni NF,  
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
XX Zhang Z;  
XX WPI; 2003-340824/32.  
XX P-PSDB; ABO25998.  
XX  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
XX and are therapeutically useful for enhancing immune responsee.  
XX  
XX Claim 2; Fig 251; 661p; English.  
XX  
XX The present invention relates to the isolation of novel human PRO  
XX polypeptides, and the polynucleotide sequences encoding them. The PRO  
XX polypeptides are secreted and transmembrane proteins. The PRO  
XX polypeptides are useful for detecting other PRO polypeptides, for linking  
XX bioactive molecules to cells expressing PRO polypeptides, for modulating  
XX biological activities of cells expressing PRO polypeptides, and for for  
XX identifying agonists or antagonists. The polynucleotide sequences  
XX encoding PRO polypeptides are useful as hybridisation probes, in  
XX chromosome and gene mapping, in the generation of antisense RNA and DNA,  
XX in the preparation of PRO polypeptides, for generating transgenic animals  
XX or knockout animals, to construct hybridisation probes for mapping the  
XX gene which encodes the PRO polypeptide, and for the genetic analysis of  
XX individuals with genetic disorders, in gene therapy, for chromosome  
XX identification, as chromosome markers, and for generating probes for PCR,  
XX Northern analysis, Southern analysis and Western analysis. The present  
XX sequence encodes a human PRO polypeptide of the invention. Note: The  
XX sequence data for this patent was obtained in electronic format directly  
XX from the USPTO web site at seqdata.uspto.gov/psipdbidentity.html  
XX  
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
SQ  
Query Match 98.2%; Score 1230; DB 8; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 6.7e-284;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 84 CTCAGAGTGGGGAATCTGGCCCTGCTGAGCGCTTCTAATAGCGCTGCTGCTGCTGCTA 143  
DB 61 CTCAGAGTGGGGAATCTGGCCCTGCTGAGCGCTTCTAATAGCGCTGCTGCTGCTA 120  
QY 144 CTGCTGCTGCTGAGCATCTGAGCGCGCTGCTGAGTGAAGCTGCTGCTGCTGCTGCTG 203  
DB 121 CTGCTGCTGCTGAGCATCTGAGCGCGCTGCTGAGTGAAGCTGCTGCTGCTGCTGCTG 180  
QY 204 GTCCCTGCTGCTGAGCATCTGAGCGCGCTGCTGAGTGAAGCTGCTGCTGCTGCTGCTG 263  
DB 181 GTCCCTGCTGCTGAGCATCTGAGCGCGCTGCTGAGTGAAGCTGCTGCTGCTGCTGCTG 240  
QY 264 GGAAGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 323  
DB 241 GGAAGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 300  
QY 324 GTGGGTGCTGATGAGAAAATTGCTCCATTTGCTCTAAAGGTGAGAAAAGAGATTCCGGT 383

DB 301 GTGGGTGCTGATGAGAAAATTGCTCCATTTGCTCTAAAGGTGAGAAAAGAGATTCCGGT 360  
QY 384 GACATAGAGCCCTGCTGCTTAAATGAGAGACCAAGGCTTCCATTTGAGTGCAGCCAGCTG 443  
DB 361 GACATAGAGCCCTGCTGCTTAAATGAGAGACCAAGGCTTCCATTTGAGTGCAGCCAGCTG 420  
QY 444 CGCAAGGCGCATCGGGAGATGAGCAACCAAGGCTTCAAGCTGAGCAGGAGCTCAAGTTG 503  
DB 421 CGCAAGGCGCATCGGGAGATGAGCAACCAAGGCTTCAAGCTGAGCAGGAGCTCAAGTTG 480  
QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGAGACGAGAGCAAGATCTACTGCTGTGAG 563  
DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGAGACGAGAGCAAGATCTACTGCTGTGAG 540  
QY 564 GAGGAGAAAGCTTACCGGAGCGCCAGCTGTCTGCTGCGAGGCGCGGAGGAGCTGAGC 623  
DB 541 GAGGAGAAAGCTTACCGGAGCGCCAGCTGTCTGCTGCGAGGCGCGGAGGAGCTGAGC 600  
QY 624 ATGCCCAAGAGAGAGGCTGCGCAATGCGCTGATGCGCGATACCTGAGCGCAAGCGGCGTG 683  
DB 601 ATGCCCAAGAGAGAGGCTGCGCAATGCGCTGATGCGCGATACCTGAGCGCAAGCGGCGTG 660  
QY 684 GCCCGTGTCTTATCGGATCAACGACCTGAGAGAGGCGCGCTTGTACTCTGAC 743  
DB 661 GCCCGTGTCTTATCGGATCAACGACCTGAGAGAGGCGCGCTTGTACTCTGAC 720  
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QY 804 GAGGAGAACTGCTGAGAGATGCTGCTGCGGCGGCTGAGAGAGAGAGAGAGAGAGAGAG 863  
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DB 841 ACCATGTACTTCATGTGTGATGATTTGAGCAAGAGAAATGATGAGCTCAAGCTGAGGCTGC 900  
QY 924 CCATTGGGGGCGCCAGATGCTCTGAGAGGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
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ID ABX79538 standard; cDNA; 1238 BP.  
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XX ABX79538;  
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XX AC ABX79538;  
XX  
XX DT 17-APR-2003 (first entry)  
XX  
XX DE Human secreted/transmembrane protein cDNA, #144.  
XX

KW	Human; gene; se; PRO; secreted; transmembrane; signal peptide;
KW	pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW	colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	US2002142961-A1.
XX	
PD	03-OCT-2002.
XX	
XX	
PF	19-NOV-2001; 2001US-00989721.
XX	
PR	16-JUN-1997; 97US-0049787P.
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PR	05-NOV-1997; 97WO-US02006.
PR	12-NOV-1997; 97US-0065186P.
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PR	24-NOV-1997; 97US-0066770P.
PR	25-FEB-1998; 98US-0075945P.
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PR	04-JUN-1998; 98US-0088021P.
PR	04-JUN-1998; 98US-0088025P.
PR	04-JUN-1998; 98US-0088026P.
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PR	10-JUN-1998; 98US-0088734P.
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PR	12-JUN-1998; 98US-0089105P.
PR	16-JUN-1998; 98US-0089440P.
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PR	17-JUN-1998; 98US-0089559P.
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PR	17-JUN-1998; 98US-0089600P.
PR	17-JUN-1998; 98US-0089653P.
PR	18-JUN-1998; 98US-0089801P.
PR	18-JUN-1998; 98US-0089907P.
PR	18-JUN-1998; 98US-0089908P.
PR	16-SEP-1998; 98WO-US019330.
PR	17-SEP-1998; 98WO-US019437.
PR	07-OCT-1998; 98WO-US021141.
PR	01-DEC-1998; 98WO-US025108.
PR	05-JAN-1999; 99WO-US000106.
PR	08-MAR-1999; 99WO-US005028.
PR	02-JUN-1999; 99WO-US012252.
PR	15-SEP-1999; 99WO-US021090.
PR	30-NOV-1999; 99WO-US028313.
PR	01-DEC-1999; 99WO-US028301.

01-DEC-1999; 99WO-US028654.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004444.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023528.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032578.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUL-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
(GETH ) GENENTECH INC.  
PA  
XX  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gertlesen ME, Goddard J, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Peoni NF,  
PI Roy MA, Stewart TN, Tumas D, Watanabe CK, Williams PM, Wood WT,  
PI Zhang Z;  
XX  
DR WP1; 2003-155950/15.  
DR P-PSDBJ; ABUS9007.  
XX  
XX  
PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
XX  
XX  
PS Claim 2; Fig 251; 647pp; English.  
XX  
XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
CC colon, lung or breast cancers) and diagnostic determination of the  
CC presence of these cancers. The PRO polypeptides are also useful as  
CC molecular weight markers or for chromosome identification. The PRO genes  
CC are useful as hybridization probes or for screening libraries of human  
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
CC therapy, particularly for replacing a defective gene. The sequences  
CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
CC amplifying and the probes detecting the PRO polynucleotides of the  
CC invention. Note: The sequence data for this patent is also available in  
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html  
XX  
XX  
Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Query Match 98.2%; Score 1230; DB 8; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 6,78-284;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGACGGGACAGACGCCCCGTTGCGCTTACGCGGCTCAGAGATTGCTGCTGCTGCG 83  
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DB 61 CTCAGAGATGAGGGGAAATCTGGCCCTTGTGGGCTTCTAATACAGCTTGGCTTCTTCA 120  
QY 144 CTGCTGCCATCTGACATCTCTCAGCGGCTGCGAGTGAAGCTGCTGCTGCTGAGATCTTC 203  
DB 121 CTGCTGCCATCTGACATCTCTCAGCGGCTGCGAGTGAAGCTGCTGCTGCTGAGATCTTC 180  
QY 204 GTCCCTGGCTTCAAAAGGGGATGCGGAGAGAAAGGAGACAAAGCGCCCGCGAGCGCT 263  
DB 181 GTCCCTGGCTTCAAAAGGGGATGCGGAGAGAAAGGAGACAAAGCGCCCGCGAGCGCT 240  
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DB 301 GTGGGTGCTCATGAAAAATTGCTCCATTTGCTTAAAGTGAGAGAAAGAGATTCGGAT 360  
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DB 361 GACATAGAGACCCCTGTGCTTAAATGAGAGAACAGGCTTCCATGTGAGTGCAGCCAGCTG 420  
QY 444 CGCAAGGCTATGGGGAGATGAGCAACAGTCTCTCACTGACCAAGAGCTCAAGTTC 503  
DB 421 CGCAAGGCTATGGGGAGATGAGCAACAGTCTCTCACTGACCAAGAGCTCAAGTTC 480  
QY 504 ATCAAGATGCTGTGCGCGGTGTCGCGAGAGAGAGCAATCTACCTGCTGATGAAG 563  
DB 481 ATCAAGATGCTGTGCGCGGTGTCGCGAGAGAGAGCAATCTACCTGCTGATGAAG 540  
QY 564 GAGGAGAAAGCGCTACGCGAGACCGCAGCTGTCTCCAGAGGCGCGGAGGACGCTGAGC 623  
DB 541 GAGGAGAAAGCGCTACGCGAGACCGCAGCTGTCTCCAGAGGCGCGGAGGACGCTGAGC 600  
QY 624 ATGCCCAAGAGAGAGGCTGCTCAATGAGCGGCTGATGCGCGCATTACTGGCGGACCGGCTG 683  
DB 601 ATGCCCAAGAGAGAGGCTGCTCAATGAGCGGCTGATGCGCGCATTACTGGCGGACCGGCTG 660  
QY 684 GCCCGTGTCTTATGAGGATCAACAGCCTGAGAGAGAGAGGCGCTTGTGCTGATCTGAC 743  
DB 661 GCCCGTGTCTTATGAGGATCAACAGCCTGAGAGAGAGAGGCGCTTGTGCTGATCTGAC 720  
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RESULT 12  
AC93559  
ID AC93559 standard; cDNA, 1238 BP.  
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XX  
16-JUN-2003 (first entry)  
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DE Novel human secreted and transmembrane protein PRO1182 cDNA.  
XX  
XX Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185;  
KW PRO943; PRO1133; PRO331; PRO1387; PRO363; PRO5723; PRO114; PRO3301;  
KW PRO9940; PRO1181; PRO7170; PRO361; PRO846; bioactive molecule; toxin;  
KW radiolabel; antibody; cell death; tissue typing; gene therapy;  
KW cytosolic; chromosome mapping; gene mapping; transgenic animal;  
KW knockout animal; immunohistochemical staining; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003022187-A1.  
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30-JAN-2003.  
XX  
14-NOV-2001; 2001US-00993667.  
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XX 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WO-US02006S.  
PR 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
XX 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
XX 28-APR-1998; 98US-0083323P.  
PR 07-MAY-1998; 98US-0084600P.  
XX 28-MAY-1998; 98US-0087106P.  
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PR 04-JUN-1998; 98US-0088021P.  
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PR 10-AUG-1998; 98US-0096012P.  
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PR 17-AUG-1998; 98US-0096757P.

PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
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PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096952P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097111P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
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PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
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PR 26-AUG-1998; 98US-0097986P.  
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PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99US-01502109P.  
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PR 11-FEB-2000; 2000US-0003565.  
PR 18-FEB-2000; 2000US-0004341.  
PR 22-FEB-2000; 2000US-0004914.  
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PR 15-MAY-2000; 2000US-0008439.  
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Best Local Similarity 100.0%; Pred. No. 6,78-284;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CTCAGAGTAGAGGGGAAATCTGGCCCTGGTGGGCGCTTCAATCAAGCTTGGCTCTCTGCA 120  
QY 144 CTGCTGCGCATCTGACATCTCTCAGCGCGGTGCGATGACGCTTGTCTGTGACATCTCTC 203  
DB 121 CTGCTGCGCATCTGACATCTCTCAGCGCGGTGCGATGACGCTTGTCTGTGACATCTCTC 180  
QY 204 GTCCCTGGCTCTCAAGGGGATGCGGGAGAGAGGAGCAAAAGCGCCCGCGAGCGGCT 263  
DB 181 GTCCCTGGCTCTCAAGGGGATGCGGGAGAGAGGAGCAAAAGCGCCCGCGAGCGGCT 240  
QY 264 GGAAGAGTCGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTCGGCGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGGTGCTCATGAG 383  
DB 301 GTGGGTGCTCATGAG 360  
QY 384 GACATAGGAG 443  
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QY 444 GCGAG 503  
DB 421 GCGAG 480  
QY 504 ATCAAG 563  
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QY 564 GAG 623  
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QY 624 ATGCGCAAG 683  
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QY 744 CACTCCCGCATGCGGAG 803  
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QY 864 ACCATGTACTCATGAG 923  
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QY 924 CCATTTGGGGGCGCCCAATGTCTCCCTGAGGGTTGGAGGAGAGAGAGAGAGAGAGAGAG 983  
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QY 1044 AAATGAG 1103

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QY 1104 TGAAG 1163  
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DT 22-APR-2003 (first entry)  
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KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; rectus pigmentum; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
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XX  
PD 06-FEB-2003.  
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PF 14-NOV-2001; 2001US-00990562.  
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Query Match 98.2%; Score 1230; DB 8; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 6,7e-284;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 84 CTCAGATGAGGGGGAATCTGCGCTTGTGGGCTTTATATCAGCTTGGCTTCTGTCA 143  
Db 61 CTCAGATGAGGGGGAATCTGCGCTTGTGGGCTTTATATCAGCTTGGCTTCTGTCA 120

Qy 144 CTGCTGCAATCTGAGCATCTCAGCGGCTGCGCATGAGCGCTGCTGTGAGATCTTC 203  
Db 121 CTGCTGCAATCTGAGCATCTCAGCGGCTGCGCATGAGCGCTGCTGTGAGATCTTC 180

Qy 204 GTCCCTGGCTCAAGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
Db 181 GTCCCTGGCTCAAGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

Qy 264 GGAAGAGTCCGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
Db 241 GGAAGAGTCCGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

Qy 324 GTGGGTGCTCATGAG 383  
Db 301 GTGGGTGCTCATGAG 360

Qy 384 GACATAG 443  
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Qy 444 GCGAAGGCTCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 503  
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Qy 504 ATCAAGAGATGCTGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
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Qy 744 CACTCCCCCATGCGGAG 803  
Db 721 CACTCCCCCATGCGGAG 780

Qy 804 GAG 863  
Db 781 GAG 840

Qy 864 ACCATGTACTCATGAG 923  
Db 841 ACCATGTACTCATGAG 900

Qy 924 CCATTGGGGGGCCCATATGCTCCCTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
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Qy 984 CAGCCAGGAG 1043  
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Qy 1044 AAACGAG 1103

Db 1021 AAACGAG 1080  
Qy 1104 TGAAG 1163  
Db 1081 TGAAG 1140

Qy 1164 CAGAAATGCTCTTCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223  
Db 1141 CAGAAATGCTCTTCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200

Qy 1224 TAGTCACTAGTAAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1253  
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XX  
DT 16-JUN-2003 (first entry)  
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XX  
KW Human; secreted and transmembrane protein; PRO; neurotrophic;  
KW neurotrophic; antiparkinsonian; cytosolic; gene therapy;  
KW chromosome mapping; gene mapping; transgenic animal; knock-out animal;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
KW gene; 88.  
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XX  
PN US2003017476-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 20-NOV-2001; 2001US-00989724.  
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PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
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PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
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Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CTCAGATGAGGGGGAATCTGGCCCTTGGTGGGCTTCTATATCAAGCTTCTCTGCA 120  
QY 144 CTGCTGACCTGACATCTCAGCGGCTGGCGATGACGCGCTGCTGTGTCAGATCTTC 203  
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QY 204 GTCCCTGCTTCAAGGGGATGCGGAGAGAGAGACAAAGGCGCCCGGACGAGCT 263  
DB 181 GTCCCTGCTTCAAGGGGATGCGGAGAGAGAGACAAAGGCGCCCGGACGAGCT 240  
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QY 324 GTGGGTGCTCATGAGAAATTTGGTCCATTTGGCTCTTAAAGTGAAGAGAGATTCGGT 383  
DB 301 GTGGGTGCTCATGAGAAATTTGGTCCATTTGGCTCTTAAAGTGAAGAGAGATTCGGT 360  
QY 384 GACATGAGACCCCTGCTGCTTATGAGAGACAGGCGCTCCATGATGATGACGAGCTG 443  
DB 361 GACATGAGACCCCTGCTGCTTATGAGAGACAGGCGCTCCATGATGATGACGAGCTG 420  
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DB 421 CGCAAGGCTATGGGAGATGAGCAACAGTCTTCACTGACCTACAGAGAGCTCAAGTTC 480  
QY 504 ATCAAGATGCTGTGCGCGGTGTGCGGAGACGAGAGAGAGATCTACCTGTGATGAG 563  
DB 481 ATCAAGATGCTGTGCGCGGTGTGCGGAGACGAGAGAGAGATCTACCTGTGATGAG 540  
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QY 864 ACCATGTAATTCATGATGAGTTTGAAGAGAGACATGTGAGCTCAAGGCTGGGCGTGC 923  
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KW Human; PRO; gene; ser; secreted polypeptide; transmembrane polypeptide;  
KW toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
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XX  
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XX  
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XX  
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PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087105P.  
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PR 03-JUN-1998; 98US-0087827P.  
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PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.

XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers I, Eaton DL,  
PI Ferrara N, Fong S, Gether H, Gerritsen ME, Goddard A, Godowski PJ  
PI Gitlin AD, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z,  
XX  
XX WPI; 2003-066810/06.  
DR P-PSDB; ABU10922.  
XX  
XX Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or

XX	antagonists of polypeptide, and as molecular weight markers.
PT	Claim 2, Fig 251, 655bp, English.
PS	The invention relates to a secreted and transmembrane polypeptide, termed
CC	PRO polypeptide, and the polynucleotide encoding it. The polypeptide is
CC	useful for detecting PRO polypeptides and for linking a bioactive
CC	molecule to a cell expressing the above polypeptides, where the bioactive
CC	molecule is a toxin, radiolabel or an antibody. The bioactive material
CC	causes the death of the cell. The polypeptide is useful for identifying
CC	agonists or antagonists of the PRO polypeptide, for preparing variants of
CC	PRO, as a molecular weight marker for protein electrophoresis purposes
CC	and the PRO polynucleotide is useful for recombinantly expressing those
CC	markers. The polynucleotide is also useful as a hybridisation probe, in
CC	chromosome and gene mapping, in generation of antisense RNA and DNA, in
CC	the preparation of PRO polypeptide, for generating transgenic animals or
CC	knockout animals which in turn are useful in the development and
CC	screening of therapeutically useful reagents, to construct hybridisation
CC	probes for mapping the gene which encodes PRO and for the genetic
CC	analysis of individuals with genetic disorders, in gene therapy, for
CC	chromosome identification, as a chromosome marker and for generating
CC	probes for PCR, Northern analysis, Southern analysis and Western
CC	analysis. This sequence represents a human PRO polynucleotide of the
CC	invention
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Query Match	98.2%; Score 1230; DB 8; Length 1238;
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 LOCUS AX403469  
 DEFINITION Sequence 356 from Patent WO0073454.  
 ACCESSION AX403469

VERSION AX403469.1 GI:21436970  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS  
 1 Aghkenazi, A. J., Baker, K. P., Botstein, D., Desnoyers, L., Baton, D., Ferrara, N., Gerber, H., Gerltzen, M., Goddard, A., Godowski, P., Grimaldi, C. O., Gurney, A. D., Kljavin, I., Napier, M. A., Pan, J., Paoni, N. F., Roy, M., Stewart, T. A., Tumas, D., Watanabe, C. K., Williams, P., Wood, W. I., and Zhang, Z.  
 Secreted and transmembrane polypeptides and nucleic acids encoding the same  
 Patent: WO 0073454-A 356 07-DEC-2000;  
 Genentech Inc. (US)  
 JOURNAL  
 TITLE  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
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 Best Local Similarity 100.0%; Pred. No. 4,5e-208;  
 Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 84 CTGAGATGAGGGGAGATCTGAGGCTGCTGAGGCTTCTATGAGCTGAGGCTTCTGCA 143  
 Qy 61 CTGAGATGAGGGGAGATCTGAGGCTGCTGAGGCTTCTATGAGCTGAGGCTTCTGCA 120  
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RESULT 3  
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LOCUS Sequence 167 from Patent WO0208284.  
DEFINITION AX454582  
ACCESSION AX454582.1 GI:21713915  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Goddard, P.J., Gunney, A.L., Hillan, K.J., Marsden, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.

TITLE  
JOURNAL  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0208284-A 167 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Goddard, Paul J. (US) ; Gunney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsden, Scott A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

FEATURES  
source  
1. 1238  
Location/Qualifiers

ORIGIN  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 98.2%; Score 1230; DB 6; Length 1238;

Best Local Similarity 100.0%; Pred. No. 4,5e-208;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 144 CTGCTGCAATCTGACATCTCAGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 203  
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Qy 204 GTCCCTGCTCCTAAAGGGATGCGGAGAGAAAGGAGCAAAAGCGCCCGGAGCGCT 263  
Db 181 GTCCCTGCTCCTAAAGGGATGCGGAGAGAAAGGAGCAAAAGCGCCCGGAGCGCT 240  
Qy 264 GGAAGAGTGGGCGGCGGAGAAAGAGACATGGGGGACAAAGGACAGAAAGGAGT 323  
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Db 1201 TAGTCAGTAGTTAAGTCCAAAAAAA 1230

RESULT 4  
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LOCUS AX491060 1238 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 167 from Patent WO200690.  
ACCESSION AX491060  
VERSION AX491060.1 GI:22323867  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
Goddard,K.P., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Pooni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.  
TITILE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0200690-A 167 03-JAN-2002;  
Genentech, Inc. (US)  
FEATURES  
SOURCE Location/Qualifiers  
1..1238  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 98.2%; Score 1230; DB 6; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 4.5e-208;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 444 CGCAAGGCCATCGGGAGATGACCAACCAAGTCTCTCAAGTGCACGAGCTCAAGTTC 503  
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Db 541 GAGAGAGCGCTACGCGACGCCAGCTGTCTCTGCCAGGCGCGGGGCGACGCTGAGC 600  
Qy 624 ATGCCCAAGAGACGAGGCTGCAATGCGCTGATGCGCGCATACCTGCGGCAAGCGGCTG 683  
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Db 661 GCCCGTCTTCAATCGGCATCAACGACCTGAGAGAGAGGCGCTTCTGTACTGTGAC 720  
Qy 744 CACTCCCCCATGCGGACCTTCAACAGTGCGCGAGCGGTGAGCCCAATGCTTACGAC 803  
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Db 901 CCAATGG 960  
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Db 1201 TAGTCAGTAGTTAAGTCCAAAAAAA 1230

RESULT 5  
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LOCUS AY358439 1238 bp mRNA linear PRI 03-OCT-2003  
DEFINITION Homo sapiens clone DNA59848 RGNL596 (UNQ596) mRNA, complete cds.  
ACCESSION AY358439  
VERSION AY358439.1 GI:37382002  
KEYWORDS FLI\_CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,



TITLE  
JOURNAL  
PUBMED  
AUTHORS  
REFERENCE  
JOURNAL  
TITLE  
JOURNAL

REMARK  
COMMENT

## FEATURES

SOURCE

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 7 Row: 9 Column: 20  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13128971.

Location/Qualifiers

1. 1248

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/db\_xref="taxon:9606"

/clone="MGC:3379 IMAGE:3507377"

/tissue\_type="Brain, neuroblastoma"

/clone\_1ib="NIH\_MGC\_19"

/lab\_host="DH10B-R"

/note="Vector: pOTB7"

1. 1248

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74. 889

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## ORIGIN

Query Match 97.8%; Score 1225.8; DB 9; Length 1248;  
Best Local Similarity 99.4%; Pred. No. 2.5e-207;  
Matches 1230; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 1 CGGCGACGACGAGGACGAGCGCCCGCTTCGCTAGCGCTGCTCAGAGTGGTGTCT 60
Qy 77 GCTTCGCTCAGAGTGAAGGAGGAAATCTGACCTGCTGAGGCGTTCTAATCAGCTGGCCTT 136
Db 61 GCTTCGCTCAGAGTGAAGGAGGAAATCTGACCTGCTGAGGCGTTCTAATCAGCTGGCCTT 120
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Db 121 CCGTCACTGCTGCTCAGAGTGAAGTCTGACCGCGCTGCGAGTGAAGCGCTGCTCTGTGCA 180
Qy 197 GATTCCTGCTCCTGCTCCTCAAGAGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256
Db 181 GATTCCTGCTCCTGCTCCTCAAGAGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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Db 481 CAAGTTCATCAAGAGAGTGTGCTGCGCGTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 540
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DEFINITION		Homo sapiens collectin sub-family member 11, transcript variant 2,	
ACCESSION		RNA (CDNA clone MGC:14216 IMAGE:4125795), complete cds.	
VERSION		BC009951	
KEYWORDS		MGC:	
SOURCE		GI:33871813	
ORGANISM		Homo sapiens (human)	
REFERENCE			
AUTHORS			
1	(bases 1 to 1417)		
1	(bases 1 to 1417)		
Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D., Alschuler,S.F., Zeeberg,B., Butow,K.H., Schaefer,C.F., Bat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J.J., Hsieh,F., Ditchenko,L., Marziani,K., Farmer,A.A., Rubin,G.M., Hong,L., Stepleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Uedlin,T.B., Tobolsky,I.S., Carimchi,P., Prange,C., Rata,S.S., Loquellano,N.A., Peters,G.U., Abramson,R.D., Mullaly,S.T., Bosak,S.A., McGowan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wozley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulys,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schnur,J., Myers,R.M., Butlerfield,Y.S., Krzywicki,M.I., Skalka,U., Smilins,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Merritt,M.A.			
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
12477932			
2	(bases 1 to 1417)		
Strausberg,R.			
Direct Submission			
Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
NIH-MGC Project URL: http://mgc.nci.nih.gov			
On Aug 19, 2003 this sequence version replaced gi:14714411.			
Contact: MGC help desk			
Email: cgapbs-remail.nih.gov			
Tissue Procurement: ATCC			
cDNA Library Preparation: Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)			
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),			
Gaithersburg, Maryland;			
Web site: http://www.nisc.nih.gov/			
Contact: nisc.mcembgri.nih.gov			
Ahter,N., Aylele,K., Beckertom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooke,S., Dietrich,N.L., Grant,S., Guan,X., Gupta,U., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R., Maduro,Q.L., Mastello,C., Masler,B., Meitlan,S.D., McCloskey,J.C., McQuinn,J., Pearson,R., Stantiprop,S., Thomas,P.J., Touchman,J.W., Tairgen,C., Vogt,J.L., Walker,M.A., Weisby,K.D., Wiggin,L.,			
REMARK COMMENT			

Young, A., Zhang, L.-H. and Green, E. D.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/BLINL at: <http://image.lnl.gov>  
Series: IRAL Plate: 20 Row: F Column: 22  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

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## ORIGIN

Query Match	92.4%	Score 1157.6;	DB 9;	Length 1417;
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Matches 1249; Conservative	0;	Mismatches 4;	Indels 79;	Gaps 1

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LOCUS	BD103302				
DEFINITION	Novel collectin.				
ACCESSION	BD103302				
VERSION	BD103302.1				
KEYWORDS	WO 0181401-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1341)				
AUTHORS	Wakamaya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.				

TITLE	Novel collection
JOURNAL	Patent: WO 0181401-A 1 01-NOV-2001; FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMITSU, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI
COMMENT	OS Homo sapiens (human) PN WO 0181401-A/1 PD 01-NOV-2001 PF 23-APR-2001 WO 2001JP003468 PR 21-APR-2000 JP 00P 120358 PI NOBUTAKA WAKAMITSU, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI
FEATURES	CC C07K44/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53 PC Novel collection FH Key FT CDS Location/Qualifiers (265)..(1077).
ORIGIN	1. .1341 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
Query Match	90.4%; Score 1132.4; DB 6; Length 1341; Best Local Similarity 99.0%; Pred. No. 8.9e-191; Matches 1139; Conservative 0; Mismatches 11; Indels 0; Gaps 0
QY	17 CGGGCCAGACACCGGACAGAGAGCCCCCGTTCGCTTAGCCGCTGTACAGAGTTGGTGTCTT 76
DB	192 CGACCCAGCGGCGGAGTGCAGCGCCCGTTCGCTTAGCCGCTCAGAGAGTTGGTGTCTT 251
QY	77 GCTTGCCTCAGATGAGGAGGAATCTGCCTGTGTGGGCGCTTCTAATCAGCGCTGACCTT 136
DB	252 GCTTGCCTCAGATGAGGAGGAATCTGCCTGTGTGGGCGCTTCTAATCAGCGCTGACCTT 311
QY	137 CCTGTCACTGTGCTCAATCTGAGACATCTCAGCCGAGCTGGCGCATGACGCTGCTCTGTGCA 196
DB	312 CCTGTCACTGTGCTCAATCTGAGACATCTCAGCCGAGCTGGCGCATGACGCTGCTCTGTGCA 371
QY	197 GATCCGTGCTCCCTGGCCCTCAAAAGGAGATGCGGAGAGAGAGAGAGCAAAAGGCGCCCGG 256
DB	372 GATCCGTGCTCCCTGGCCCTCAAAAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
QY	257 ACGGCTTGGAAGAGTGGGCGCCACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 316
DB	432 ACGGCTTGGAAGAGTGGGCGCCACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
QY	317 AGGCAAGTGGGTGCTGATGAGAAATTTGGTCCATTTGGCTCTTAAAGTGTGAAGAGAGAG 376
DB	492 AGGCAAGTGGGTGCTGATGAGAAATTTGGTCCATTTGGCTCTTAAAGTGTGAAGAGAGAG 551
QY	377 TTCCGATGATAGAGACCCCTGGTCTCTTAATGAGAAACAGGAGCTCCCATGTGAGTGCAG 436
DB	552 TTCCGATGATAGAGACCCCTGGTCTCTTAATGAGAAACAGGAGCTCCCATGTGAGTGCAG 611
QY	437 CCAAGCTGCGAAGGCGCATCGGAGAGATGAGACACAGGTCTTCACTGATGACGAGGAGCT 496
DB	612 CCAAGCTGCGAAGGCGCATCGGAGAGATGAGACACAGGTCTTCACTGATGAGGAGGAGCT 671
QY	497 CAAATTCAATCAAGAAATCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 556
DB	672 CAAATTCAATCAAGAAATCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
QY	557 GGTGAAGAGAGAGAGGCTACGCGGACGCGCCAGCTGCTCTGACAGAGGCGCGGAGGAGCAG 616
DB	732 GGTGAAGAGAGAGAGGCTACGCGGACGCGCCAGCTGCTCTGACAGAGGCGCGGAGGAGCAG 791
QY	617 GCTGAGATGCTCCAGAGAGAGAGGCTGCTGATGAGTGGCTGATGAGTGGCTGATGAGTGGCT 676
DB	792 GCTGAGATGCTCCAGAGAGAGAGGCTGCTGATGAGTGGCTGATGAGTGGCTGATGAGTGGCT 851
QY	677 CGGAGCTGAGCGCGGTGTCTTCAATGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736



Db	852	GGGCGCGCCGGTGTCTTTCATGTGGGATCAACGACTGGAGAGAGGGCGCTTGTGTGA	911
Qy	737	CTCTGACCACTCCCCATGCGGACCTTTCACAAATGGCGGACGGGTGAGCCCCAACATGC	796
Db	912	CTCTGACCACTCCCCATGCGGACCTTTCACAAATGGCGGACGGGTGAGCCCCAACATGC	971
Qy	797	CTACGACGAGGAGGACTCGGTGGAAATGGTGGCCCTCGGGCGGCTGGAAACGACGTGGCCTG	856
Db	972	CTACGACGAGGAGGACTCGGTGGAAATGGTGGCCCTCGGGCGGCTGGAAACGACGTGGCCTG	1031
Qy	857	CCACACACACATGTACTTCATGTGTGAAGTTTACAGAGGAAACATGTGAGCCTCAGGCTG	916
Db	1032	CCACACACACATGTACTTCATGTGTGAAGTTTACAGAGGAAACATGTGAGCCTCAGGCTG	1099
Qy	917	GGGCTGCCCATTTGGGGGGCCCAATGTCCTCGCAGGGTTGGCAGGAGCAGAGCCCAAGAC	976
Db	1092	GGGCTGCCCATTTGGGGGGCCCAATGTCCTCGCAGGGTTGGCAGGAGCAGAGCCCAAGAC	1155
Qy	977	ATGTGTGCCACGACGAGGAGCTGTCCCTCTGTGAAGGTGAGGCTCACTGAGTAGAGGCT	1033
Db	1152	ATGTGTGCCACGACGAGGAGCTGTCCCTCTGTGAAGGTGAGGCTCACTGAGTAGAGGCT	1211
Qy	1037	GTTGTCTAAACTGAGAAAATGAGCTATGCTTAAGAGGAAAATGAAAGTGTCTGGGGTG	1099
Db	1212	GTTGTCTAAACTGAGAAAATGAGCTATGCTTAAGAGGAAAATGAAAGTGTCTGGGGTG	1277
Qy	1097	CTGTCTCGAAGACAGAGTTTCACTTACTGTATTGTAGCCCAATGTCAATTATGTAT	1156
Db	1272	CTGTCTCGAAGACAGAGTTTCACTTACTGTATTGTAGCCCAATGTCAATTATGTAT	1333
Qy	1157	TATTACCCAG 1166	
Db	1332	TATTACCCAG 1341	
RESULT 9			
BD103330			
LOCUS	BD103330	1269 bp	DNA linear PAT 27-AUG-2002
DEFINITION	Novel collectin.		
ACCESSION	BD103330		
VERSION	BD103330.1 GI:22648904		
KEYWORDS	WO 0181401-A/29.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1. (bases 1 to 1269)		
JOURNAL	Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.		
	Novel collectin		
	Patent: WO 0181401-A 29 01-NOV-2001;		
	FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI		
	KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI		
COMMENT	OS Homo sapiens (human)		
	PN WO 0181401-A/29		
	PD 01-NOV-2001		
	PF 23-APR-2001 WO 2001JP003468		
	PI 21-APR-2000 JP 00P 120358		
	PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI		
	SAKAMOTO,		
	PI YUICHIRO KISHI		
	PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53		
	CC Novel collectin		
	PH Key		
	FT CDS		
FEATURES			
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
ORIGIN			
Query Match	78.1%;	Score 978.4;	DB 6; Length 1269;
Best Local Similarity	92.8%;	Pred.No. 1.8e-163;	

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 DB 1200 CTGCTCTGAAGAGCAGAGTTTCACTTACTGTAATTGAGCCCAATGCTATTATTAAT 1259  
 QY 1157 TATTACCCAG 1166  
 DB 1260 TATTACCCAG 1269  
 RESULT 10  
 BD103331  
 LOCUS Novel collectin. 1269 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Novel collectin.  
 ACCESSION BD103331  
 VERSION BD103331.1 GI:22648905  
 KEYWORDS WO 0181401-A/30.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 1269)  
 TITLE Wakamiya,N., Keshi,H., Ocani,K., Sakamoto,T. and Kishi,Y.  
 JOURNAL Novel collection  
 Patient: WO 0181401-A 30 01-NOV-2001;  
 FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI  
 KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YOICHIRO KISHI  
 OS Homo sapiens (human)  
 PN WO 0181401-A/30  
 PD 01-NOV-2001  
 PF 23-APR-2001 WO 2001JP003468  
 PR 21-APR-2000 JP 00P 120358  
 PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
 SAKAMOTO,  
 YOICHIRO KISHI  
 PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
 CC Novel collectin  
 FH Key  
 FT CDS Location/Qualifiers  
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 FEATURES  
 source  
 ORIGIN  
 Query Match 78.1%; Score 978.4; DB 6; Length 1269;  
 Best Local Similarity 92.8%; Pred. No. 1.8e-163;  
 Matches 1067; Conservative 0; Mismatches 11; Indels 72; Gaps 1;  
 QY 17 CGGGCCAGCAGCGGCGAGAGCGCCCGTTCGCTGAGCGGCTGAGAGTTGGTCTCT 76  
 DB 192 CGAGCGAGCGGCGAGAGCGCCCGTTCGCTGAGCGGCTGAGAGTTGGTCTCT 251  
 QY 77 GCCTCGCTCAGAGATGAGGAGGATCTGAGCCCTGCTGAGGCTTCAATCAGCTGAGCTT 136  
 DB 252 GCCTCGCTCAGAGATGAGGAGGATCTGAGCCCTGCTGAGGCTTCAATCAGCTGAGCTT 311  
 QY 137 CCTGTCACTGTGCTCATCTGAGCATCTCAAGCGGCTGCGAGTGAAGCGCTGCTGTGCA 196  
 DB 312 CCTGTCACTGTGCTCATCTGAGCATCTCAAGCGGCTGCGAGTGAAGCGCTGCTGTGCA 371  
 QY 197 GATCTCTGCTCTGCGCTCAAGGAGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256  
 DB 372 GATCTCTGCTCTGCGCTCAAGGAGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431  
 QY 257 ACGGCTGAG 316  
 DB 432 ACGGCTGAG 462  
 QY 317 AGGAGAGTGGGTGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 376  
 DB 463 -----AAAGGTGAG 479

QY 377 TTCCGGTGAATATGAGACCCCTGCTGCTTAATGAGAGACAGAGCTCCCATGTGAGTGAG 436  
 DB 480 TTCCGGTGAATATGAGACCCCTGCTGCTTAATGAGAGACAGAGCTCCCATGTGAGTGAG 539  
 QY 437 CCAGCTGCGAG 496  
 DB 540 CCAGCTGCGAG 599  
 QY 497 CAAGTTCAATCAGAGATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGAGAGAGAGAGAG 556  
 DB 600 CAAGTTCAATCAGAGATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGAGAGAGAGAGAG 659  
 QY 557 GGTGAAG 616  
 DB 660 GGTGAAG 719  
 QY 617 GCTGAGCATGCGCCAG 676  
 DB 720 GCTGAGCATGCGCCAG 779  
 QY 677 CGGCTGCGCGCGGTGTGCTTCAATGCGCATCAACAGACTGAGAGAGAGAGAGAGAGAG 736  
 DB 780 CGGCTGCGCGCGGTGTGCTTCAATGCGCATCAACAGACTGAGAGAGAGAGAGAGAGAG 839  
 QY 737 CTGTCACCACTCCCGCATGCGGAGCTTCAACAGAGTGGCGGAGAGAGAGAGAGAGAGAG 796  
 DB 840 CTGTCACCACTCCCGCATGCGGAGCTTCAACAGAGTGGCGGAGAGAGAGAGAGAGAGAG 899  
 QY 797 CTAAG 856  
 DB 900 CTAAG 959  
 QY 857 CCACAGCAG 916  
 DB 960 CCACAGCAG 1019  
 QY 917 GGGCTGCGCATGAG 976  
 DB 1020 GGGCTGCGCATGAG 1079  
 QY 977 ATGAGTGCAGCAG 1036  
 DB 1080 ATGAGTGCAGCAG 1139  
 QY 1037 GTTGTCTTAATCTAG 1096  
 DB 1140 GTTGTCTTAATCTAG 1199  
 QY 1097 CTGCTCTGAAG 1156  
 DB 1200 CTGCTCTGAAG 1259  
 QY 1157 TATTACCCAG 1166  
 DB 1260 TATTACCCAG 1269  
 RESULT 11  
 BD103303  
 LOCUS Novel collectin. 1139 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Novel collectin.  
 ACCESSION BD103303  
 VERSION BD103303.1 GI:22648877  
 KEYWORDS WO 0181401-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 1139)  
 TITLE Wakamiya,N., Keshi,H., Ocani,K., Sakamoto,T. and Kishi,Y.  
 JOURNAL Novel collection  
 Patient: WO 0181401-A 2 01-NOV-2001;





QY 530 CGAGACGAGACGACGATCTACCTGCTGCTGTAAGGAGAGAGCGCTACGCGGAGCGCCA 589  
Db 431 CGAGACGAGACGACGATCTACCTGCTGCTGTAAGGAGAGAGCGCTACGCGGAGCGCCA 490  
QY 530 GCTGTCCTGACGAGGCGCGGCGGAGCGCTGAGTACGAGTACGAGGAGCGCTGAGTACG 649  
Db 491 GCTGTCCTGACGAGGCGCGGCGGAGCGCTGAGTACGAGTACGAGGAGCGCTGAGTACG 550  
QY 650 CTTGATGCGCGGATCTCTGAGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709  
Db 551 CTTGATGCGCGGATCTCTGAGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610  
QY 710 CTTGATGAGAGAGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769  
Db 611 CTTGATGAGAGAGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 670  
QY 770 GTGAGCGAGCGGCTGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829  
Db 671 GTGAGCGAGCGGCTGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730  
QY 830 CTTGAGCGGCGGCTGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889  
Db 731 CTTGAGCGGCGGCTGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 790  
QY 890 CAAGAGAGACATGTGAGCGCTGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949  
Db 791 CAAGAGAGACATGTGAGCGCTGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850  
QY 950 AGGCTGCGAGGAGCAGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009  
Db 851 AGGCTGCGAGGAGCAGAGCGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 910  
QY 1010 GGGTGGAGGCTCAGTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069  
Db 911 GGGTGGAGGCTCAGTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970  
QY 1070 GAGGAAATGAAGTGTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1129  
Db 971 GAGGAAATGAAGTGTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030  
QY 1130 ATTGTAGCCCAATGCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1166  
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LOCUS BD103329 1197 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel collectin.  
ACCESSION BD103329.1 GI:22648903  
VERSION WO 0181401-A/28.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1197)  
Wakamaya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.  
TITLE Novel collectin  
AUTHORS Patent: WO 0181401-A 28 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI  
KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI  
OS Homo sapiens (human)  
PN WO 0181401-A/28  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI  
SAKAMOTO, YUICHIRO KISHI  
PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53  
CC Novel collectin  
FH Key Location/Qualifiers

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Source (265).. (933).  
Location/Qualifiers  
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ORIGIN  
Query Match 66.6%; Score 834.4; DB 6; Length 1197;  
Best Local Similarity 86.5%; Pred. No. 5.9e-138;  
Matches 995; Conservative 0; Mismatches 11; Indels 144; Gaps 1;  
17 CGAGCGCGAGCGGCGAGCG 76  
Db 192 CGAGCGCGCGAGCGGCGAGCG 251  
QY 77 GCCTGCGCGCGAGCGGCGAGCG 136  
Db 252 GCCTGCGCGCGAGCGGCGAGCG 311  
QY 137 CTTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196  
Db 312 CTTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371  
QY 197 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256  
Db 372 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390  
QY 257 ACAGCGCTGGAAGAGTCCG 316  
Db 391 ----- 390  
QY 317 AGGCGAGTGTGGT 376  
Db 391 ----- AAAGTGAAGAGAGA 407  
QY 377 TTCGGTGAATGAAGACCG 436  
Db 408 TTCGGTGAATGAAGACCG 467  
QY 437 CGAGCTGCGAGAGCG 496  
Db 468 CGAGCTGCGAGAGCG 527  
QY 497 CAAGTTCATGAAGATGT 556  
Db 528 CAAGTTCATGAAGATGT 587  
QY 557 GGTGAAGAGAGAGAGCG 616  
Db 588 GGTGAAGAGAGAGAGCG 647  
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Db 648 GCTGAGCATGCCCAAGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 707  
QY 677 CGGCTGCG 736  
Db 708 CGGCTGCG 767  
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QY 857 CCACACCAACATGATCTCATGT 916  
Db 888 CCACACCAACATGATCTCATGT 947  
QY 917 GGGCTGCCCATTTGGGGCG 976

Db	948	GGGCTGGCCATTGGGGGGCCCA	CAATGTCCCTGCAAGGTTGGCAGGGA	CAGAGCCCAAGC	1007
Qy	977	ATGCTGCGCAAGCAGGAGACTG	TCCTCTGTGTGAAGGTGAGGCTCA	CTGAGTAGAGGCT	1036
Db	1008	ATGGTGCCAGCGCAGGAGCTGT	CCCTCTGTGAAGGTGAGGCTCA	CTGAGTAGAGGCT	1067
Qy	1037	GTTGTCTAACTGAGAAAATGG	CCCTATTAAGAGAAAATGA	AAAGTTCCTGGGGTG	1096
Db	1068	GTTGTCTAACTGAGAAAATGG	CCCTATTAAGAGAAAATGA	AAAGTTCCTGGGGTG	1127
Qy	1097	CTGTCTGGAAGACAGATTCA	TCACTGTATTTAGCCCCCATG	CTATTATGTAT	1156
Db	1128	CTGTCTGGAAGACAGATTCA	TCACTGTATTTAGCCCCCATG	CTATTATGTAT	1187
Qy	1157	TATTATCCAG	1166		
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RESULT	14				
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LOCUS	BD103306				
DEFINITION	BD103306				
ACCESSION	BD103306	1067 bp	DNA	linear	PAT 27-AUG-2002
VERSION	BD103306.1				
KEYWORDS	GI:22648880				
SOURCE	WO 0181401-A/5.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				

REFERENCE	1 (bases 1 to 1067)
AUTHORS	Wakamuta, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.
TITLE	Novel collection
JOURNAL	Patent: WO 0181901-A 5 01-NOV-2001; FUJO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMUTA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI
COMMENT	OS Homo sapiens (human)

**COMMENT**

PF	23-APR-2001 WO 2001JP003468	
PR	21-APR-2000 JP 00P 120358	
PI	NOBUATAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI	
SAKAMOTO,		
PI	YUICHIRO KISHI	
PC	C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/531	
CC	Novel	collectin
PH	Key	Location/Qualifiers
FT	CDS	(141). . (803).

FEATURES	location/Qualifiers
source	1..1067
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**ORIGIN**

Query Match	66.4%	Score 832.2;	DB 6;	Length 1067;
Best Local Similarity	96.8%	Pred. No. 1.5e-137;		
Matches 849; Conservative	0;	Mismatches 28;	Indels 0;	Gaps 0

QY	230	AGGAGACATGCGGGGACAAAGGACAGAAAGGACAGTGTGGGTCGTCATGAGAAATTTGGTCC	349
Db	191	AGGGGATTCGGGAGAGAAAGGAGACAAAGGCGCCCCGACGGCTGTGAGAAATCGGCC	250
QY	350	CATTGGCTTAAAGGTGAGAAAGGAGATTCCGGTGCATATAGACCCCCCTGTCTAATGG	409
Db	251	CACGGGAGAAAAAGGTGAGAAAGGAGATTCCGGTGACATAGACCCCCCTGTCTAATGS	310
QY	410	AGAACCAAGGCTCCCATGTGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGAGATGACAA	469
Db	311	AGAACCAAGGCTCCCATGTGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGAGATGACAA	370
QY	470	CCAGGTCTCTACGCTGACCAAGCGAGCTCAAGTTTATCAAGAAATGCTGTGCCCCGAGTGG	529

Db	371	CCAGGTCTCTAGCTGACCGACGAGACTCAAGTTTCAACGAATGCTGTGCGCGGTGTGGC	430
Qy	530	CGAGCGGAGGCAAGATCTACCTTCTGTGAAGAGGAAGCCCTTACCGGACGCCCA	589
Db	431	CGAGCGGAGGCAAGATCTACTTCTGTGAAGAGGAAGCCGCTTACCGGACGCCCA	490
Qy	590	GCTGTCCTGCCAGGGCCGCGGGGGGACGCTGAGCAATGCCCAAGACGAGGCTTCCCAATGG	649
Db	491	GCTGTCCTGCCAGGGCCGCGGGGGGACGCTGAGCAATGCCCAAGACGAGGCTTCCCAATGG	550
Qy	650	CCTGATGGCCGCAATCTGTGGCGCAAGCGGGCCCTGGCCGGTGCCTTATCGGCATCAACGA	709
Db	551	CCTGATGGCCGCAATCTGTGGCGCAAGCGGGCCCTGGCCGGTGCCTTATCGGCATCAACGA	610
Qy	710	CCTGGAGAAAGAGGGGCGCTTCTGTGATCTGTGACCACTTCCCAATGCGGACCTTCAACAA	769
Db	611	CCTGGAGAAAGAGGGGCGCTTCTGTGATCTGTGACCACTTCCCAATGCGGACCTTCAACAA	670
Qy	770	GTGGCGCAGCGGTGAGCCCAACATATGCTTACGACGAGAGGAGACTGGCTGGAGATGTGTGGC	829

Db 671 GTGGCGGACGGCTGAGCCCAACATGCTGCTACGACGAGGAGGACTGGCGCTGAC 730

Qy 830 CTGGGGGGGCGCTGGAACGACGTGGGCTGCTCAACACCATGACTTCAATGTGTGACTTGA 889

Db 731 CTGGGGCGGCTGGAACGACGTGGGCTGCTCAACACCATGACTTCAATGTGTGACTTGA 790

Qy 890 CAAGAGAACAATGTGAGCCTTCAGGCTGCGGCTGCGCAATGGGGGCCCCACACATGTCTCC 949

Oy	950	AGGGTTGGCAGGGGACAGAGCCCAACATAGTGTGCAGCAGAGGAGCGTCCCTCTGGAA	1009
Db	851	AGGTTGGCAGGGGACAGAGCCCAACATAGTGTGCAGCAGAGGAGCGTCCCTCTGGAA	910
Oy	1010	GGGTGGAGGCTCACTGAGTAGAGGGCTGTGTTCTTAACTGAGAAATGGCCCTATGCTTAA	1069
Db	911	GGGTGGAGGCTCACTGAGTAGAGGGCTGTGTTCTTAACTGAGAAATGGCCCTATGCTTAA	970

**Db**

Db	971	GAGGAAATGAAAGTGTCTCGGGGTGCTGCTGAAGAAGCAGAGTTCATTACCTGT	1030
Qy	1130	ATTGTAGCCCCAATGTCATTATGTAATTAATTAACCAAG	1166
Db	1031	ATTGTAGCCCCAATGTCATTATGTAATTAATTAACCAAG	1067

RESULT 15			
BD103332			
LOCUS	813 bp	DNA	linear
DEFINITION	Novel collectin.		
ACCESSION	BD103332		
VERSION	BD103332.1 GI:22648906		

## KEYWORDS

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 813)  
AUTHORS  
Makaniy, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.  
TITLE  
Novel collectin  
JOURNAL  
Patent: WO 0181401-A 31 01-NOV-2001;

**COMMENT**

PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBITAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI  
SAKAMOTO,  
PI YUICHIRO KISHI

Search completed: December 16, 2004, 19:01:41  
Job time : 8745 secs

PC C07K14/47.C12N15/12.C12P21/02.A01K67/027.C07K16/18.G01N33/53  
CC Novel collectin Location/Qualifiers  
FH Key 1..813  
FT source /organism='Homo sapiens (human)'.  
FT Location/Qualifiers  
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/db\_xref="taxon:9606"

## ORIGIN

Query Match 64.9%; Score 813; DB 6; Length 813;  
Best Local Similarity 100.0%; Pred. No. 3.8e-134; Mismatches 0; Indels 0; Gaps 0;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	121	TAATCAGCCTGCGCTTCTCTGCACTGCTGCATCTTGAGCATCTCAGCCGAGCTGGCGATG	180
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QY	781	GTGAGCCCCAACATATCCCTTACGACGAGAGAAATGCTGTGAGATGTTGGCTTCGGGCGGCT	840
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QY	841	GGAACGACGTGGGCTGGCCACACCAACATATCTTATGTGATGTTTACAAGAGAAACA	900
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QY	961	GGACGAGCCCGAGACCATGTGACCGCAGGGAGTGTCCCTCTGTGAAGGGTGGAGGCT	1020
Db	963	GGACGAGCCCGAGACCATGTGACCGCAGGGAGTGTCCCTCTGTGAAGGGTGGAGGCT	1022
QY	1021	CACTGAGTAGAGGGCTGTGTCTTAAACTGAGAAAAATGGCTATGCTTAAAGAGAAATGA	1080
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QY	1081	AAGGTTCCTGGGGGCTGTCTCTGAGAAACAGATTTCAATACCTGTATTTGATGCCCC	1144
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QY	1141	AATGCAATGATGATATATATTCACCAAGATTGCTCTCCATCAATTAAGCTTGCTTGTC	1200
DB	1143	AATGTCATATGATATATATATATCCAGAAATTCCTTCCATTAAGCTTGCTTGTC	1202
QY	1201	AGTATATCAATTAATATCTTTAAGTAGTGACAGTAGTAAATGTC	1245
DB	1203	AGTATATCAATTAATATCTTTAAGTAGTGACAGTAGTAAATGTC	1247
RESULT 2	CR604552	1252 bp	linear
LOCUS	CR604552	full-length cDNA clone	CSDDC024YP19 of Neuroblastoma Cot
DEFINITION	25-normalized of Homo sapiens (human).		
ACCESSION	CR604552.1	GI:50485359	
VERSION	CR604552		
KEYWORDS	HTC; CNSLT_CDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Li,W.B., Gruber,C., Jeehee,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
REMARK	Contact : Peng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1252)		
REFERENCE	Genoscope.		
AUTHORS	Direct Submission		
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secrete@genoscope.cns.fr		
JOURNAL	- Web : www.genoscope.cns.fr)		
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		
FEATURES	Location/Qualifiers		
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QY	121	TAAATCAGCTCGGCGCTTCTCTGTCACTGTGTGCATCTGAGATCTCCAGCCGAGTGGCATG	180
DB	135	TAAATCAGCTCGGCGCTTCTCTGTCACTGTGTGCATCTGAGATCTCCAGCCGAGTGGCATG	194
QY	181	ACGCTGTCTGTGACAGATCTGTCTCCCTGAGCTCAAGGGGATGCGGAGAGAGAGAG	240
DB	195	ACGCTGTCTGTGACAGATCTGTCTCCCTGAGCTCAAGGGGATGCGGAGAGAGAGAG	254
QY	241	ACAAAGCGCGCGCGCGAGCGGCTGGAAGAGTCCGCCCAAGGAGAAAGAGACATCG	300
DB	255	ACAAAGCGCGCGCGCGAGCGGCTGGAAGAGTCCGCCCAAGGAGAAAGAGACATCG	314

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OY 301 GGGACAAAGACAGAAAGGACAGTGTGGGTCGTATGAGAAAAATGTGCTCCATTGGCTCTA 360
DB 315 GGGACAAAGACAGAAAGGACAGTGTGGGTCGTATGAGAAAAATGTGCTCCATTGGCTCTA 374
OY 351 AAGGTGAGAAAGAGATTCCTGGGTGACATAGAGACCCCTGTGTCTTAATGAGAACAGAGCC 420
DB 375 AAGGTGAGAAAGAGATTCCTGGGTGACATAGAGACCCCTGTGTCTTAATGAGAACAGAGCC 434
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DB 435 TCCCATGTGAGTGCAGCCAGCTGCGGACAGGACCAATGGGGAGATGAGCAACAGGTCTCTC 494
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OY 1141 AATGTCAATATTAATTAATTAACCAAGATTTGCTTTCAATAAGCTTGTGCTTGTCCA 1200
DB 1155 AATGTCAATATTAATTAATTAACCAAGATTTGCTTTCAATAAGCTTGTGCTTGTCCA 1214
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DB 1215 AGCTATTAACAATAATCTTAAGTGTGAGATGATTA 1252

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RESULT 3      CR599770      1150 bp      mRNA      linear      HMC 21-JUL-2004
DEFINITION   Full-length cDNA clone CS0DC018YD07 of Neuroblastoma Cot
ACCESSION    CR599770
VERSION      CR599770.1 GI:50480577
KEYWORDS     HTC; cNSLT_cDNA.

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 1150)
AUTHORS     Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.lifetech.com/ Invitrogen Corporation 1600
            Faraday Avenue
            Genoscope.
            2 (bases 1 to 1150)
REFERENCE   Direct Submission
AUTHORS     Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE       BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr
JOURNAL     - Web : www.genoscope.cns.fr)
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
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Beet Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 288 AAAGAGACATGGGGGACAAAGAGACAGAAAGGACAGTGTGGGTCGTATGAGAAAAATGTG 347
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DB 403 AACCAAGTCTCTGAGCTGACAGAGAGCTCAAGTTCATCAAGAAATGCTGTGCGCGGTG 462
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OY 588 CAGCTGTCTTCGACAGGCGCGGAGGACGCTGAGACATGCCAAGAGAGAGAGAGAGAGAG 647
DB 523 CAGCTGTCTTCGACAGGCGCGGAGGACGCTGAGACATGCCAAGAGAGAGAGAGAGAGAG 582
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 962)  
NIH-MGC <http://img.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
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Plate: LNCM2088 row: f column: 15  
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Location/Qualifiers

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insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 56.3%; Score 705; DB 5; Length 962;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 755; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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529 GCGAGACGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 588  
121 GCGAGACGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 180  
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181 AGCTGTCTGCGAGGCG 240  
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211 GCGTATGCGCGCAATCTGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
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301 ACCTGAGAGAGAGGCG 360  
769 AGTGCGCAGCGCGGTGAGCGCAATGCTTACGAGAGAGAGAGAGAGAGAGAGAGAG 828  
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VERSION BQ927000  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 962)  
NIH-MGC <http://img.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
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<http://image.llnl.gov>  
Plate: LNCM2562 row: j column: 14  
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Location/Qualifiers

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source

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EcoRI; CDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 54.0%; Score 676; DB 5; Length 962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCGCAGCAGCGGAGAGCGCCGCTTGCCTAGCGGCTGCTCAGAGATTGTGTCGTC 78



RESULT 8  
 BF206254  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

BF206254 672 bp mRNA linear EST 06-NOV-2000  
 601865264F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4098278 5',  
 mRNA sequence.  
 BF206254  
 BF206254.1 GI:11099840  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (Bases 1 to 672)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strusberg, Ph.D.  
 Email: [cs9abds-remail.nih.gov](mailto:cs9abds-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at: [image.llnl.gov](http://image.llnl.gov)  
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/notes="Organ: brain; Vector: pGB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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Best Local Similarity	100.0%; Pred. NO. 0;
Matches 645; Conservative	0; Mismatches 0; Indels 0; Gaps 0

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QY	76	TGCTTCGCGCTCAGGATGAGGGGAAATCTGGCTCTGGTGGGCGTTCTAATCAGCTGGCCT	135
Db	61	TGCTTCGCGCTCAGGATGAGGGGAAATCTGGCTCTGGTGGGCGTTCTAATCAGCTGGCCT	120
QY	136	TCCTGTCACTGCGCCATCTGGACATTCCTCAGCGCGGCTGGGGATGAGCGCCCTGCTGTGC	195
Db	121	TCTGTTCATCTGTGCGCATTTGGACATTCCTCAGCGCGGCTGGGGATGAGCGCCCTGCTGTGC	180
QY	196	AGATCTCGTCCCTTGCGCTCAAAAGGGGATGTGGGAGAGAGAGAGACAAAGCGCCCCG	255
Db	181	AGATCTCGTCCCTTGCGCTCAAAAGGGGATGTGGGAGAGAGAGAGAGACAAAGCGCCCCG	240
QY	256	GATCGGCTTGGAGAGTCCGCGCCCACTGGAGAGAGAGAGAGAGATGGGGAGACAAAGACAG	315
Db	241	GATCGGCTTGGAGAGTCCGCGCCCACTGGAGAGAGAGAGAGAGATGGGGAGACAAAGACAG	300
QY	316	AAGCAGTGTGGGTGCTCATGGAAAAATTGGCCCATGGCTTAAAGGTGAGAAAGAG	375
Db	301	AAGCAGTGTGGGTGCTCATGGAAAAATTGGCCCATGGCTTAAAGGTGAGAAAGAG	360

OY	376	ATTCGGATGATAGGACCCCTGTCTCTTAATGAGAAACAGAGCCCTCATGTGATGCA	435
Db	361	ATTCCGTGACATAGACCCCTCTGTCTTAATGAGAAACAGAGCCCTCATGTGATGCA	420
OY	436	GCCAGCTCCGCAAGCCCATTCGGGGAGATGGAACAACAGGTCTCTCACTGACCAAGCGAGC	495
Db	421	GCCAGCTCCGCAAGCCCATTCGGGGAGATGGAACAACAGGTCTCTCACTGACCAAGCGAGC	480
OY	496	TCAAGTTATCAAGATGCTGTGCGCGGTGTGCGGAGCGGAGAGCAAGATCTACCTGC	555
Db	481	TCAAGTTATCAAGATGCTGTGCGCGGTGTGCGGAGCGGAGAGCAAGATCTACCTGC	540
OY	556	TGTGTGAAGAGAGAGAGCGCTTACGGGAGCGCCAGCTGTCTTGCCAGGGCCCGGGGGCA	615
Db	541	TGTGTGAAGAGAGAGAGCGCTTACGGGAGCGCCAGCTGTCTTGCCAGGGCCCGGGGGCA	600
OY	616	CGCTGAGCATGCCCAAGAGCAGAGCTGCCAATGGGCTGATGGCCG	660
Db	601	CGCTGAGCATGCCCAAGAGCAGAGCTGCCAATGGGCTGATGGCCG	645

RESULT 9	
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DEFINITION	BE383325 640 bp mRNA linear EST 21-JUL-2000
ACCESSION	6012969236F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628448 5',
VERSION	BE383325
KEYWORDS	BE383325
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 640)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strauberg, Ph.D.

Email: [cgabds-r@mail.nih.gov](mailto:cgabds-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
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 Location/Qualifiers

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/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN		
Query Match	49.6%;	Score 622; DB 2; Length 640;
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Db	1	ACGGCCCGCTTGCCTTAGCGCGCTGCTCAGAGATTGGTGTCTCGCTGCGCTCAGAGATGAGG 60

QY	96	GGGAATCTGGCCCTGGATGGGGGTTCTTAATCAAGCCCTGACCTTCCTGTCACTGCTGGCACT	155
Db	61	GGGAATCTGGCCCTGGATGGGGGTTCTTAATCAAGCCCTGACCTTCCTGTCACTGCTGGCACT	120
QY	156	GGACATCTTCAGCCGGCTGGCGGATGACGCTTGCTGTGTGACAGATCTTCGTCCCTGGCCTC	215
Db	121	GGACATCTTCAGCCGGCTGGCGGATGACGCTTGCTGTGTGACAGATCTTCGTCCCTGGCCTC	180
QY	216	AAAGGGGATGGGGGAGAGAAAGGAGACAAAGCCGCCCCCGACGGCCCTGGAAAGAGTGGGC	275
Db	181	AAAGGGGATGGGGGAGAGAAAGGAGACAAAGCCGCCCCCGACGGCCCTGGAAAGAGTGGGC	240
QY	276	CCCAACGGGAGAAAAAGAGACATGGGGGACAAAGAGACAGAAAGCAGTGGGTGTCAT	335
Db	241	CCCAACGGGAGAAAAAGAGACATGGGGGACAAAGAGACAGAAAGCAGTGGGTGTCAT	300
QY	336	GGAAAAATTTGGTCCCATTTGGCTCTTAAAGTGTGAAAGAGATTCGGGTGACATAGAACCC	395
Db	301	GGAAAAATTTGGTCCCATTTGGCTCTTAAAGTGTGAAAGAGATTCGGGTGACATAGAACCC	360
QY	396	CCTGGTCTTAATGGAAGAACCAAGCCTCCCATGTGATGACAGCTGCGCAAGGCCATC	455
Db	361	CCTGGTCTTAATGGAAGAACCAAGCCTCCCATGTGATGACAGCTGCGCAAGGCCATC	420
QY	456	GGGGAGATGGAACAACCAAGTCTCTCAGCTGACCAAGGACCTCAAGTTATCAAGAAATGCT	515
Db	421	GGGGAGATGGAACAACCAAGTCTCTCAGCTGACCAAGGACCTCAAGTTATCAAGAAATGCT	480
QY	516	GTCGCGCGGTGTGCGCGGAGACGGAGAGCAAGATCTACCTGTGTGTGAGAGAGAGAGCGC	575
Db	481	GTCGCGCGGTGTGCGCGGAGACGGAGAGCAAGATCTACCTGTGTGTGAGAGAGAGAGCGC	540
QY	576	TACGCGGACGCCCAAGTCTCTGCGCAAGGGCCGCGGGGGGACGGCTGACATGCCCAAGAC	635
Db	541	TACGCGGACGCCCAAGTCTCTGCGCAAGGGCCGCGGGGGGACGGCTGACATGCCCAAGAC	600
QY	636	GAGGCTGCACATGGCCTGATGG	657
Db	601	GAGGCTGCACATGGCCTGATGG	622

RESULT	10
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DEFINITION	BZ62656 644 bp mRNA linear EST 26-OCT-2000 60115146S1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3507377 5' , mRNA sequence.
ACCESSION	BZ62656
VERSION	BZ62656.1 GI:9135855
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 644) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1995) Contact: Robert Strausberg, Ph.D.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

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	Query Match	100.0%	Score 622;	DB 2;	Length 644;
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			Indels	0;	Gaps 0;
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Oy	76	TGCTTGCGCTCAGGATGAGGGGGAATCGGCCCTGTGGCGTTCTAATCAGCCGTGGCT	135		
Db	83	TGCTTGCGCTCAGGATGAGGGGGAATCGGCCCTGTGGCGTTCTAATCAGCCGTGGCT	142		
Oy	136	TCCGTGACAGCTGCTCCATCTGSAATCATCTCAGCGCGGTGGGATGAGCGCTGCTGTGC	195		
Db	143	TCCGTGACAGCTGCTCCATCTGSAATCATCTCAGCGCGGTGGGATGAGCGCTGCTGTGC	202		

196	AGATCTCTGTCCTCCGAGCTCAAAAGGGGATGCGGAGAAAGGAGACAAAGGCGCGCCCG	255
203	AGATCTCTGTCCTCCGAGCTCAAAAGGGGATGCGGAGAAAGGAGACAAAGGCGCGCCCG	262
256	GACGGCTTGGAAAGTGGCGCCCAACGGAGAAAAAGAGACATGGGGGACAAAGGACGA	315
263	GACGGCTTGGAAAGTGGCGCCCAACGGAGAAAAAGAGACATGGGGGACAAAGGACGA	322
316	AAGCAGTGTGGGTCGTATGGAAAAATTGGTCCATTGGCTCTTAAAGTGAAGAAAGAG	375
323	AAGCAGTGTGGGTCGTATGGAAAAATTGGTCCATTGGCTCTTAAAGTGAAGAAAGAG	382
376	ATTCCGGTGAATGAGACCCCTTGCTCTTATGGAGAACAGGCTTCCATGTGATGCA	435
383	ATTCCGGTGAATGAGACCCCTTGCTCTTATGGAGAACAGGCTTCCATGTGATGCA	442
436	GCCAGCTGCGAAGGCCATGGGGAGATGAGCAACCGATGCTCTCAGTGCACAGCGAGC	495
443	GCCAGCTGCGAAGGCCATGGGGAGATGAGCAACCGATGCTCTCAGTGCACAGCGAGC	502
496	TCAAGTTCATCAAGATGTGTGCGCCGGTGTGCGCGAGACGGAGACGAATCTTACCTGC	555
503	TCAAGTTCATCAAGATGTGTGCGCCGGTGTGCGCGAGACGGAGACGAATCTTACCTGC	562
556	TGTTGAAGAGAGAGAGAGCGCTTACGCGGACGCTTGTCTTGCAAGGGCGCGGGGGCA	615
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616	CGCTGAGCATGCCAAGGACGA	637
623	CGCTGAGCATGCCAAGGACGA	644

RESULT 11	
LOCUS	BE382845
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ACCESSION	601297714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627794 5',
VERSION	BE382845
KEYWORDS	mRNA sequence.
SOURCE	BE382845.1 GI:9328210
	EST.
	Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 723)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: [image.lnl.gov](http://image.lnl.gov)  
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EcoRI; CDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library."

Query Match 49.5%; Score 620; DB 2; Length 723;  
Best Local Similarity 100.0%; Pred. No. 1.4e-304; Indels 0; Gaps 0;  
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1 ACGCCCGCTCGCTAGCGCGCTCTCAGAGTGTGTCCTGCGCTCAGATGAGG 60  
96 GGGATTCGCGCTCGCTGAGGCTCTTAATCAGCTGCGCTTCTGTCACCTGCGCATCT 155  
61 GGGATTCGCGCTCGCTGAGGCTCTTAATCAGCTGCGCTTCTGTCACCTGCGCATCT 120  
156 GGACATCTCAGCGCGCTGAGGCTCTGTCAGATCTGTCCTGCGCTCAGATGAGG 215  
121 GGACATCTCAGCGCGCTGAGGCTCTGTCAGATCTGTCCTGCGCTCAGATGAGG 180  
97 AAAAGGAGTGGGAG 275  
216 AAAAGGAGTGGGAG 240  
181 AAAAGGAGTGGGAG 240  
276 CCCACGGAG 335  
241 CCCACGGAG 300  
98 GGAATTAATTTGGTCCATTGGCTCTAAGGTGAGAAAGGAGATTCCGGTGACATAGAG 395  
336 GGAATTAATTTGGTCCATTGGCTCTAAGGTGAGAAAGGAGATTCCGGTGACATAGAG 360  
301 GGAATTAATTTGGTCCATTGGCTCTAAGGTGAGAAAGGAGATTCCGGTGACATAGAG 360  
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361 CTTGTCTTAATGAGAACCAAGGCTCTCCATGTGAGTGAGGACAGCTGGAGAGCCATC 420  
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456 GGGGAGATGAGAACCAAGGCTCTCTCAGCTGACACGAGCTCAAGTTCAATCAAGATGCT 515  
421 GGGGAGATGAGAACCAAGGCTCTCTCAGCTGACACGAGCTCAAGTTCAATCAAGATGCT 480  
99 GTCCCGGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 575

DB 481 GTCCGCGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
576 TACGCGAG 635  
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99 GAGGCTGCAATGAGCTGAT 655  
601 GAGGCTGCAATGAGCTGAT 620

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DEFINITION mRNA sequence.  
ACCESSION BF312666  
VERSION BF312666.1 GI:11260511  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 613)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: [image.lnl.gov](http://image.lnl.gov)  
Plate: LNCM108 row: p column: 15  
High quality sequence stop: 612.  
Location/Qualifiers  
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/note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library."

ORIGIN  
Query Match 48.9%; Score 613; DB 2; Length 613;  
Best Local Similarity 100.0%; Pred. No. 5.1e-301; Indels 0; Gaps 0;  
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GCGGCGAG 60  
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99 TCTGTCACTGCTGAGATCTGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195  
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found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
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Location/Qualifiers

## FEATURES

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/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 47.3%; Score 593; DB 2; Length 715;  
Best Local Similarity 100.0%; Pred. No. 8.2e-291;  
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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156 GGAATCTGCGCTGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCTAT 215  
121 GGAATCTGCGCTGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCTAT 180  
216 AAGGGGATGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 275  
181 AAGGGGATGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
276 CCCAGGGAG 335  
241 CCCAGGGAG 300  
336 GGAATCTGCGCTGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCTAT 395  
301 GGAATCTGCGCTGCGCTTCTAATCAGCTGCGCTTCTGCTCACTGCTGCTAT 360  
396 CCTGTCTAATGAG 455  
361 CCTGTCTAATGAG 420  
456 GGGGATGGAG 515  
421 GGGGATGGAG 480  
516 GTCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 575  
481 GTCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
576 TACGCGAGCGCCAGAGTCTCTGCGAGGCGCGGGGCGACGCTGAGCATGCC 628  
541 TACGCGAGCGCCAGAGTCTCTGCGAGGCGCGGGGCGACGCTGAGCATGCC 593

RESULT 15  
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DEFINITION mRNA sequence.  
ACCESSION BF311185

VERSION BF311185.1 GI:1125873  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE 1 (bases 1 to 702)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
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High quality sequence stop: 695.  
Location/Qualifiers

## FEATURES

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/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 46.9%; Score 588; DB 2; Length 702;  
Best Local Similarity 100.0%; Pred. No. 2.9e-288;  
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 GCGGGCCAGGAG 75  
1 GCGGGCCAGGAG 60  
76 TGCGGCGCTCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135  
61 TGCGGCGCTCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
136 TCCTGTCACTGCTCAGATCTGAGATCTGAGCGGCTGAGGATGAGCGCTTGTGC 195  
121 TCCTGTCACTGCTCAGATCTGAGATCTGAGCGGCTGAGGATGAGCGCTTGTGC 180  
196 AGATCTGTGCTCCTGCGCTTCAAAGGGAGTGGGAGAGAGAGAGAGAGAGAGAG 255  
181 AGATCTGTGCTCCTGCGCTTCAAAGGGAGTGGGAGAGAGAGAGAGAGAGAGAG 240  
256 GACGGGCTGAG 315  
241 GACGGGCTGAG 300  
316 AAGGAGTGTGGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375  
301 AAGGAGTGTGGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
376 ATTCGGGATGAG 435  
361 ATTCGGGATGAG 420  
436 GCGAGTGGCGAG 495

Db 421 GCCAGCTGCCAAGGCCATCGGGAGATGACAAACAAGTCTTCAAGCTGACGAGC 480  
QY 496 TCAAGTTCATCAGAGATGCTGTGCGCGTGTGCGGAGACGAGAGCAAGATCTACCTGC 555  
Db 481 TCAAGTTCATCAGAGATGCTGTGCGCGTGTGCGGAGACGAGAGCAAGATCTACCTGC 540  
QY 556 TGGTGAAGAGAGAGAGCGCTACCGGACGCCCAAGCTGTCTGCGCAGG 603  
Db 541 TGGTGAAGAGAGAGAGCGCTACCGGACGCCCAAGCTGTCTGCGCAGG 588

Search completed: December 17, 2004, 03:37:43  
Job time : 6193 secs



GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 11:20:00 ; Search time 3865 Seconds  
(without alignments)  
2555.024 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 271

Sequence: 1 MRGNLAVGVILSLAFSL.....NDVACHTTMYPCPEKXNM 271

Scoring table:  
OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65644297

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

MODEL=frame+ p2n.model -DEV=xlp  
-Q=/sgn2.1/USPRO pool P/US09806277/runcat.15122004.101701.29764/app.query.fasta\_1.455  
-DB=EST -QFWT=fastcat -SUFFIX=oligo.rst -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCLALIGN=200 -THR.SCOR=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NOR=ext -REASIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09806277.QCGN.1.1.6425.qruncat.15122004.101701.29764 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG.SCOR=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:\*

1: gb\_est1:\*\n2: gb\_est2:\*\n3: gb\_hcc:\*\n4: gb\_est3:\*\n5: gb\_est4:\*\n6: gb\_est5:\*\n7: gb\_est6:\*\n8: gb\_g981:\*\n9: gb\_g982:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271	100.0	1252	3	CR604552 full-length
2	271	100.0	1397	3	CR612268 full-length
3	208	76.8	894	5	BU147034 AGENCOURT
4	205	75.6	1150	3	CR599770. full-length
5	202	74.5	962	3	BQ927000 AGENCOURT
6	195	72.0	1083	5	BK427124 AGENCOURT
7	190	70.1	672	2	BF206254 AGENCOURT
8	189	69.7	640	2	BE383325 AGENCOURT
9	188	69.4	723	2	BE382845 AGENCOURT

10	182	67.2	644	2	BE262656
11	181	66.8	683	2	BE382433
12	180	66.4	715	2	BE313199
13	179	66.1	613	2	BF312666
14	175	64.6	654	2	BE312923
15	175	64.6	1012	2	BE260904
16	172	63.5	737	2	BE313410
17	172	63.5	767	2	BE260355
18	171	63.1	702	2	BE311185
19	168	62.0	788	2	BF311981
20	164	60.5	962	5	BQ069775
21	162	59.8	542	2	BE313758
22	159	58.7	537	2	BE261686
23	157	57.9	525	2	BE261369
24	136	50.2	769	2	BE312920
25	123	45.4	538	2	BE312003
26	119	43.9	823	4	B1198782
27	119	43.9	916	2	BF316717
28	114	42.1	893	2	BF314316
29	113	41.7	1078	5	EX333394
30	109	40.2	892	2	BF314275
31	109	40.2	1094	4	BM547424
32	104	38.4	665	2	BF317432
33	104	38.4	1321	2	BF316150
34	95	35.1	626	2	BF316496
35	95	35.1	728	2	BE260359
36	94	34.7	642	1	AV655586
37	87	32.1	948	2	BF206235
38	83	30.6	273	5	BK099011
39	83	30.6	1195	2	BF316270
40	81	29.9	969	5	BK427123
41	75	27.7	924	4	B1198572
42	74	27.3	1071	5	CB992054
43	71	26.2	851	6	B1199068
44	70	25.8	619	4	BF311988
45	67	24.7	642	2	BF311988

## ALIGNMENTS

RESULT 1  
LOCUS CR604552 1252 bp mRNA linear HTC 21-JUL-2004  
DEFINITION Full-length cDNA clone CS0DC024Y19 of Neuroblastoma Cot  
25-normalized of Homo sapiens (human).  
ACCESSION CR604552  
VERSION CR604552.1 GI:50485359  
KEYWORDS HTC; CNSL; cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE Li M.B., Gruber C., Jessee J. and Polayes D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
CONTACT : Feng Liang Email : fliang@lifestech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1252)  
REFERENCE Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with NotI and cloned  
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life technologies, a  
division of Invitrogen.  
FEATURES  
location/Qualifiers  
1..1252  
/organism="Homo sapiens"

ORIGIN

/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clone="CS0DM008YL18"  
/tissue\_type="Neuroblastoma Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

## Alignment Scores:

Pred. No.: 8 46e-251 Length: 1252  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277a-6 (1-271) x CR604552 (1-1252)

QY 1 MetAArgGlyAenLeuAlaLeuValGlyValLeuLeuLeuLeuAphLeuSerLeuLeu 20  
Db 104 ATGAGGGGGAAATCTGGCCCTGGTGGGCGTTCTAATCAAGCCTGGCCTTCTGTCAGTCTG 163  
QY 21 ProSerGlyHisProGlnProAlaGlyAAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 164 CCATCTGGACATCTCTCAAGCCGGCTGGCGATGACCGCTCTGTGCAATCTGTCCTCT 223  
QY 41 GlyLeuLeuGlyAAspAlaGlyGlyValGlyAAspLeuGlyAlaProGlyAAspProGlyAAsp 60  
Db 224 GGCTTCAAGAGGAGATGCGGAG 283  
QY 61 ValGlyProThrGlyGlyValGlyAAspMetGlyAAspLeuGlyGlyValGlySerValGly 80  
Db 284 GTCCGGCCCGGAG 343  
QY 81 ArgHisGlyValIleGlyProIleGlySerLeuGlyValGlyAAspSerGlyAAspIle 100  
Db 344 CGTATGGAGAAATTTGGTCCATTGGCTCTAAGAGTGAAGAGAGAGATCCGGTGAATATA 403  
QY 101 GlyProProGlyProAenGlyGlyProGlyLeuProCysGlyCysSerGlnLeuAArg 120  
Db 404 GGACCCCTGGTCTTAATGAG 463  
QY 121 AlaIleGlyGlyMetAAspAenGlnValSerGlnLeuThrSerGlnLeuLeuValIle 140  
Db 464 GCCATCGGGAG 523  
QY 141 AsnAlaValAlaGlyValAArgGlyThrGlySerValIleTyrLeuLeuValGlyGlyGlu 160  
Db 524 AATCTGTGCGCGGTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583  
QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyAArgGlyGlyThrLeuSerMetPro 180  
Db 584 AAGGGCTACGGGAG 643  
QY 181 LysAAspGlnAlaAlaAenGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 644 AAGGACAG 703  
QY 201 ValPheIleGlyIleAenAAspLeuGlyValGlyValAlaPheValTyrSerAAspHisSer 220  
Db 704 GTCTTCAATCGGATCAACAG 763  
QY 221 ProMetAArgThrPheAenLeuValTyrAArgSerGlyGlyProAAsnAlaTyrAAspGlyGlu 240  
Db 764 CCCATCGGAG 823  
QY 241 AspCysValAlaGlyMetValAlaSerGlyGlyTyrAAspValAlaCysValIleThrMet 260  
Db 824 GACTGCTGAG 883  
QY 261 TyrPheMetCysGlyPheAAspLeuGlyAAspMet 271  
Db 884 TACTTCAATGTGTGAGTTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916

## RESULT 2

CR612268 1397 bp mRNA linear HTC 21-JUN-2004  
LOCUS full-length cDNA clone CS0DM008YL18 of Fetal liver of Homo sapiens  
(human)

ACCESSION CR612268  
VERSION CR612268.1 GI:50493075  
KEYWORDS HTC; cDNA; cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1397)

## REFERENCE

AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

## COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
1. 1397

## FEATURES

source  
/organism="Homo sapiens"  
/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clone="CS0DM008YL18"  
/tissue\_type="Fetal liver"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

## Alignment Scores:

Pred. No.: 9.37e-251 Length: 1397  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-806-277a-6 (1-271) x CR612268 (1-1397)

QY 1 MetAArgGlyAAspLeuAlaLeuValGlyValLeuLeuLeuAphLeuSerLeuLeu 20  
Db 92 ATGAGGGGGAAATCTGGCCCTGGTGGGCGTTCTAATCAAGCCTGGCCTTCTGTCAGTCTG 151  
QY 21 ProSerGlyHisProGlnProAlaGlyAAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 152 CCATCTGGACATCTCTCAAGCCGGCTGGCGATGACCGCTCTGTGCAATCTGTCCTCT 211  
QY 41 GlyLeuLeuGlyAAspAlaGlyGlyValGlyAAspLeuGlyAlaProGlyAAspProGlyAAsp 60  
Db 212 GGCTTCAAGAGGAGATGCGGAG 271  
QY 61 ValGlyProThrGlyGlyValGlyAAspMetGlyAAspLeuGlyGlyValGlySerValGly 80  
Db 272 GTCCGGCCCGGAG 331  
QY 81 ArgHisGlyValIleGlyProIleGlySerLeuGlyValGlyAAspSerGlyAAspIle 100  
Db 332 CGTATGGAGAAATTTGGTCCATTGGCTCTAAGAGTGAAGAGAGAGATCCGGTGAATATA 391  
QY 101 GlyProProGlyProAenGlyGlyProGlyLeuProCysGlyCysSerGlnLeuAArg 120  
Db 392 GGACCCCTGGTCTTAATGAG 451

Qy 121 AAlaIleGlyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIleLeu 140  
Db 452 GCCATCCGGGAGATGGACCAACAGGTCTCTCGCTGACGACGAGACTCAAGTTCATCAAG 511  
Qy 141 AAsnAlaValAlaGlyValArgGluThrGluSerLeuValIleTyrLeuLeuValIleGluGlu 160  
Db 512 AATGCTGTGCGCGGTGTGCGGAGACGAGACCAAGATCTTACTCTGCTGTGAAGAGAGAG 571  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
Db 572 AAGCGCTACGGCGAGCCCGACAGTGTCTGTCCAGCGGCGCGGGGACACCTGAGCATGCC 631  
Qy 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 632 AAGGACGAGGCTGCGCAATGGCTGTATGGCCGCTCTGGCGCAGCCGCGCTGCGCT 691  
Qy 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
Db 692 GTCTTCATCGGCATACAGACCTGAGAGAGAGGAGGCGCTTCTGTACTGTGACCATCTCC 751  
Qy 221 ProMetArgThrPheAsnLysTyrArgSerGlyGluProAsnAsnAlaTyrAspGluGlu 240  
Db 752 CCCATGCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTACGACGAGAGAG 811  
Qy 241 AspCysValGluMetValAlaSerGlyTyrPheAspValAlaCysHisThrThrMet 260  
Db 812 GACTGCGTGGAGATGTGTGGCTCTGGCGGCTGGAGACGATGGCTGTGCACACCATG 871  
Qy 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 872 TACTTCATGTGTGAGTTTGAACAAGAGAACATG 904

RESULT 3  
BU147034 894 bp mRNA linear EST 03-SEP-2002  
LOCUS BU147034  
DEFINITION AGENCOURT\_8736281 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6338772  
5', mRNA sequence.  
ACCESSION BU147034  
VERSION BU147034.1 GI:22660566  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 894)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgsapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LNCM2532 row: 1 column: 13  
High quality sequence stop: 621.  
Location/Qualifiers  
1. 894  
/organism="Homo sapiens"  
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/tissue\_type="neuroblastoma, cell line"  
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/clone\_lib="NIH\_MGC\_47"  
/note="Organ: brain; Vector: pOTB7, site\_1: XhoI; site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G). Size-selected >500bp for average

Insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 4,2e-190 Length: 894  
Score: 208.00 Matches: 242  
Percent Similarity: 99.18% Conservative: 0  
Best Local Similarity: 99.18% Mismatches: 1  
Query Match: 76.75% Indels: 2  
DB: Gaps: 0  
US-09-806-277a-6 (1-271) x BU147034 (1-894)

Qy 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
Db 72 ATGAGGGGGAATCTGGCCCTGTGTGGCTTAAATCAAGCTTGACCTTCTCTCACTGCTG 131  
Qy 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
Db 132 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACCGCTGTCTGTGTGACAGATCCTGCTCCT 191  
Qy 41 GlyLeuLysGlyAspAlaGlyValGlyLysGlyAspLysGlyValProGlyValArgPro 60  
Db 192 GGCCTCAAGGGGATGTGGGAGAGAGAGAGACAAAGGCGCCCGGACCGCTGGAGAGA 251  
Qy 61 ValGlyProThrGlyGluLysGlyAspMetGlyAspLysGlyValGlyValGlySerValGly 80  
Db 252 GTCCGCCCCACGGAGAGAGAGAGAGACATGGGGAGCAAGAGACAGAGAGAGAGAGAGAG 311  
Qy 81 ArgHisGlyLysIleGlyProIleGlySerIleGlyLysGlyLysGlyAspSerGlyAspIle 100  
Db 312 CGTATGGAGAAATTTGGTCCATTTGGCTCTTAAAGTGAGAAAGAGATTCGGTGACATTA 371  
Qy 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyCysSerGlnLeuAlaGly 120  
Db 372 GGACCCCTGTGTCTTAAATGAGAACAGGCTCCCATGTGTGTGACAGCCACTCGCCAG 431  
Qy 121 AAlaIleGlyGluMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuPheIleLeu 140  
Db 432 GCCATCCGGGAGATGGACCAACAGGTCTCTTACTGACGACGAGCTCAAGTTCATCAAG 491  
Qy 141 AAsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValIleGluGlu 160  
Db 492 AATGCTGTGCGCGGTGTGCGGAGACGAGACCAAGATCTTACTCTGTGTGAAGAGAGAG 551  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180  
Db 552 AAGCGCTACGGCGAGCGCCAGCTGTCTTCCGACAGGCGCGGGGACAGCTGAGCATGCC 611  
Qy 181 LysAspGluAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
Db 612 AAGACGAGGCTGCGCAATGGCTGTATGGCCCAATACCTTGGGCAAGCCGCGCTGCGCT 671  
Qy 201 ValPheIleGlyIleAsnAspLeuGluLysGluGlyAlaPheValTyrSerAspHisSer 220  
Db 672 GTCTTCATCGGCATACAGACCTGNA-GAAGAGGGGCGCTTGTGTACTGTGACCATCTC 730  
Qy 220 rProMetArgThrPheAsnLysTyrArgSerGlyGluProAsnAsnAlaTyrAspGluGlu 240  
Db 731 CCCCATGCGGACCTTCAACAGTGGCGAGCGGTGAGCCCAACATGCTTACGACGAGAGA 790  
Qy 240 uAspCysVal 243  
Db 791 GCACTGCGGTG 800  
RESULT 4  
CR599770 1150 bp mRNA linear HTC 21-JUL-2004  
LOCUS CR599770  
DEFINITION full-length cDNA clone CS0DC018Y007 of Neuroblastoma C6c

ACCESSION	25-normalized of Homo sapiens (human).
VERSION	CRS99770
KEYWORDS	CRS99770.1 GI:50480577
SOURCE	HTC; CNSTL_cDNA.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 1150)
JOURNAL	L.I.W.B., Gruber,C., Jeesee,J. and Polayes,D.
REMARK	Full-length cDNA libraries and normalization Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600 Paradise Avenue 2 (bases 1 to 1150) Genoscope. Direct Submission Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of invitrogen
FEATURES	Location/Qualifiers
source	1..1150 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSDDC018YD07" /tissue_type="Neuroblastoma Cot 25-normalized" /plasmid="pCMVSPORT_6"
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Alignment Scores:	
Pred. No.:	4.19e-187 Length: 1150
Score:	205.00 Matches: 205
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatch: 0
Query Match:	75.65% Indels: 0
DB:	Gaps: 0
US-09-806-277A-6 (1-271) x CRS99770 (1-1150)	
Dy	67 LyeglyAspmecGlyAspLyaglyGlnlygSerValGlyArgHisGlyLyseIlegly 86
Dd	223 AAAGAGCAATCGGGGAGCAAAGAGCAAGAAGGCACTGTGGTCGCATGAAAAATTGCT 282
Dy	87 ProilegyseryLygLygLnlygLyaspseryAspIleglyProPrgLyproasn 106
Dd	283 CCCATTGGCTCTAAAGTGAGTAAGAAAGAAATTCGGGTGACATAGACCCTGTCCTAAT 342
Dy	107 GlynlpurroglyLeupProcyGlnCybeserGlnleuArglyAlalleglylmetasp 126
Dd	343 GGAGAACCAAGGCCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGGAATGAC 402
Dy	127 AsngInvalserGlnleuthSerGlnleuPheIlelyBAANAAlavalAglyVal 146
Dd	403 AACCAAGCTCTTCACTACCAAGCAAGCTCAAGTTTCATCAAGAAATCTGTGCGCGGTG 462
Dy	147 ArgglunthrgluseryIetyrleuleuVallysgjucjnulyBarglytralAaspAla 166
Dd	463 CGCAGAGACGAGAGACAATCTACTGCTGTGTGAAGAGGAGAAAGCGCTACGCGAGACGCC 522
Dy	167 GlnleuserCygsinglyArgglylythrleusernetPrcolyBAPglualAlaasn 186
Dd	523 CAGCTGTCTTCCACGGGGCCGGGGGACCGCTGAGCATGCCAAGACGAGAGCTGCCAAT 582
Dy	187 GlyleumetalaaIetyrleualaglAlaglyleuAlaArgValPheIleglyTlleasn 206
Dd	583 GGCTGTATGCGCGCATCTTGGCGCACCGGCGCTGGCCGTCGTTCATCGGCAATCAC 642

QY	207	AsplenigluysglnuglvalalapevalTYrSerAspiiserPrometcgttrPheasn	226
Db	643	GACCTGGAGNAGGAGGGCGCCTTGCTGTACTCTGACCACTCCCGCATCGACCTTACAC	702
QY	227	LYsTPrTgSerGlygluProAsnAsnAlaTYrAspGlnuLubpCyValGluMetVal	246
Db	703	AMGTGGCGACGGGTGAGCCCAACATGCTCTAGACGAGGAGCATGCTGAGATGCTG	762
QY	247	AlaSerGlygluTYrPpanAspValAlaCYeHIsphrThrMetTYrPheMetCYeGluPhe	266
Db	763	GCCCTGGCGCGCTGGAAAGACAGTGGCTGCACACCACTGATCTTCACTGATGAGTTT	822
QY	267	AsplysgluAsnMet	271
Db	823	GACNAGGAGAACATG	837
RESULT 5			
LOCUS	BQ927000	962 bp	mRNA linear EST 20-AUG-2002
DEFINITION	AGENCOURT 8804355 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377965		
ACCESSION	BQ927000		
KEYWORDS	BQ927000.1 GI:22342031		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euteheria; Primates; Carnivora; Homnidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: LNCM562 row: 1 column: 14		
	High quality sequence stop: 616.		
FEATURES	Location/Qualifiers		
source	1..962		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:6377965"		
	/tissue_type="neuroblastoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_idb="NIH_MGC_47"		
	/note="Organ: brain; Vector: pOTB7, Site 1: XhoI, Site 2:		
	ECORI; cDNA made by oligo-dT priming. Directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adaptor: GGCACGAG(G). Size-selected >500bp for average		
	insert size 1.8kb. Library constructed by Ling Hong in		
	the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: this is a NIH_MGC Library."		
ORIGIN			
Alignment Scores:			
Pred. No.:	2.8e-184	Length:	962
Score:	202.00	Matches:	202
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	74.54%	Indels:	0
DB:	5	Gaps:	0

QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
 DB 72 ATGAGGGGAAATCTGCGCTGGTGAGCGCTTCTAAATCAGCTGGCCCTTCTGTCACTGCTG 131  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
 DB 132 CCATTTGGAACATCTCAGCGGCTGGCCATGACGCTGCTCTGTGCAATCTCTGCTCCCT 191  
 QY 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
 DB 192 GGCCTCAAGGGGAGATGCGGAG 251  
 QY 61 ValGlyProThrGlnGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
 DB 252 GTCCGCCCCACGGGAG 311  
 QY 81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
 DB 312 CGTCAATGAGAAATTTGGTCCATTTGGCTCTAAAGTGAGAGAGAGAGAGAGAGAGAGAT 371  
 QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProGlyValGlyValGlyValGlyVal 120  
 DB 372 GGACCCCTGCTGCTAAATGAG 431  
 QY 121 AlaIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 140  
 DB 432 GCCATCGGAGAGATGAG 491  
 QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
 DB 492 AATGCTGTCCGCGGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551  
 QY 161 LysArgGlyValAlaAspAlaGlnLeuSerCySerGlnGlyValGlyValGlyValGly 180  
 DB 552 AAGGCTTACGCGGAG 611  
 QY 181 LysAspGlyValAlaAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 200  
 DB 612 AAGGAG 671  
 QY 201 ValPhe 202  
 DB 672 GTCTTT 677  
 DB  
 RESULT 6  
 LOCUS BX427124 1083 bp mRNA linear EST 04-MAY-2004  
 DEFINITION BX427124 Homo sapiens FETAL LIVER Homo sapiens cDNA clone  
 CSQDM008Y18 5-PRIME, mRNA sequence.  
 ACCESSION BX427124  
 VERSION BX427124.2 GI:47002248  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1083)  
 L1,W.B., Gruber,C., Jeessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 Contact: Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with NotI and cloned  
 into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 This sequence belongs to sequence cluster 1719.f  
 For more information about this cluster, see

http://www.genoscope.cns.fr/cdna7a=CSQDM008DP09QP1&c=1719.f.  
 FEATURES  
 Location/Qualifiers  
 1..1083  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSQDM008Y18"  
 /tissue\_type="FETAL LIVER"  
 /dev\_stage="fetal"  
 /clone\_lib="Homo sapiens FETAL LIVER"  
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-Oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with NotI and  
 cloned into the NotI and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,79e-177 Length: 1083  
 Score: 195.00 Matches: 262  
 Percent Similarity: 98.87% Conservative: 0  
 Best Local Similarity: 98.87% Mismatches: 2  
 Query Match: 71.96% Indels: 3  
 DB: 5 Gaps: 0

US-09-806-277a-6 (1-271) x BX427124 (1-1083)  
 QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
 DB 92 ATGAGGGGAAATCTGCGCTGGTGAGCGCTTCTAAATCAGCTGGCCCTTCTGTCACTGCTG 151  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCySerValGlnIleLeuValPro 40  
 DB 152 CCATTTGGAACATCTCAGCGGCTGGCCATGACGCTGCTCTGTGCAATCTCTGCTCCCT 211  
 QY 41 GlyLeuValGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 60  
 DB 212 GGCCTCAAGGGGAGATGCGGAG 271  
 QY 61 ValGlyProThrGlnGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
 DB 272 GTCCGCCCCACGGGAG 331  
 QY 81 ArgHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 100  
 DB 332 CGTCAATGAGAAATTTGGTCCATTTGGCTCTAAAGTGAGAGAGAGAGAGAGAGAGAGAT 391  
 QY 101 GlyProProGlyProAsnGlyGluProGlyLeuProGlyValGlyValGlyValGlyVal 120  
 DB 392 GGACCCCTGCTGCTAAATGAG 451  
 QY 121 AlaIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 140  
 DB 452 GCCATCGGAGAGATGAG 511  
 QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
 DB 512 AATGCTGTCCGCGGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571  
 QY 161 LysArgGlyValAlaAspAlaGlnLeuSerCySerGlnGlyValGlyValGlyValGlyVal 180  
 DB 572 AAGGCTTACGCGGAG 631  
 QY 181 LysAspGlyValAlaAsnGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 200  
 DB 632 AAGGAGAGAGAGATGCGGAG 690  
 QY 201 ValPheIleGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 220  
 DB 691 GTCTTCAATGAG 750  
 QY 221 ProMetArgThrPheAsnLysTrpArgSerGlyGluProAsnAlaValGlyValGlyValGly 240

Db 751 CCCATGCGGACCTTCAACAGTGGCGSMG-GGTGGAGCCCAACATGCTTACGACGAGA 809  
 Qy 240 uapgcYValaGluMetValaAlaSerGlyGlyTTPAspValaAlaCysH1stHrThrme 260  
 Db 810 GGACTGGGTGAGTGGTGGCTTGGGCGGCTGGAACGAGCTGGCTTCCACACACCAT 869  
 Qy 260 tTy-PheMetCys 264  
 Db 870 GTACTTCATGTGT 882  
 RESULT 7  
 BF206254  
 LOCUS  
 DEFINITION  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 672)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: L1CM964 row: 0 column: 15  
 High quality sequence stop: 670.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4098278"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"  
 /note="Organ: brain; Vector: pOTB7; Site: 1: XhoI; Site 2:  
 EcoRI; CDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,72e-173 Length: 672  
 Score: 190.00 Matches: 190  
 Percent Similarity: 100.00% Conservatave: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 70.11% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-806-277A-6 (1-271) x BF206254 (1-672)

Qy 1 MetATGtYAsnLeuAlaLeuValaGlyValleuIeserLeuAlaPheLeuSerLeu 20  
 Db 75 ATGAGGGGGAATCTGGCTTGGTGGGCTTCAACAGCTGGCTTCTGTCATCTGTG 134  
 Qy 21 ProSerGlyAspProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 135 CCATCTGGACATCTCAGCCGGCTGGCGATGACGCTGTGTGTCAGATCTCGTCCCT 194

Qy 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyValaProGlyLysProGlyLys 60  
 Db 195 GGCTTCMAAGGAGGATGCGGAG 254  
 Qy 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlyLysGlySerValGly 80  
 Db 255 GTTCGGCCCCCAGGAG 314  
 Qy 81 ArgH1sGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
 Db 315 CGTCATGAAATAATTGTCCTCCATGCTCTAAAGGTGAGAGAGAGAGATCCCGTGCATCA 374  
 Qy 101 GlyProProGlyLysProAsnGlyGlyProGlyLysProGlyLysProGlyLysProGlyLys 120  
 Db 375 GAGACCCCTGTCCTTATGAG 434  
 Qy 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlyLysPheIleLys 140  
 Db 435 GCCTATGGGAGATGAGACACAGAGCTCTCAAGCTGACAGAGAGAGAGAGAGAGAGAGAGAG 494  
 Qy 141 AsnAlaValaAlaGlyValaArgGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 160  
 Db 495 AATGCTGTGCGCGTGTGCGGAG 554  
 Qy 161 LysArgTyrAlaAspAlaGlnLeuSerGlyGlnGlyLysGlyLysGlyLysGlyLysGlyLys 180  
 Db 555 AAGCGCTACGCGAG 614  
 Qy 181 LysAspGlyAlaAlaAsnGlyLeuMetAla 190  
 Db 615 AAG 644

RESULT 8  
 BE383325  
 LOCUS  
 DEFINITION  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 640)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: L1CM913 row: 9 column: 09  
 High quality sequence stop: 638.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3628448"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"  
 /note="Organ: brain; Vector: pOTB7; Site: 1: XhoI; Site 2:  
 EcoRI; CDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-CDNA synthesis kit

FEATURES  
 source

## ORIGIN

(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## Alignment Scores:

Pred. No.: 6,82e-172 Length: 640  
Score: 189.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.74% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277a-6 (1-271) x BE383325 (1-640)

OY 1 MetatrgtGlyAanleuAlaleuValGlyValleuIleSerleuAlapheluSerleu 20  
Db 55 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATACAGCTGGCTTCTGTCATGCTG 114  
OY 21 ProserGIyHISProGIInProAlaGlyAapAapAlaCySerValGlnIleleuValPro 40  
Db 115 CCATCTGACATCTCCACCGCGCTGCGCATGACGCTGCTGTGCAAGATCTCTGCTCT 174  
OY 41 GlyleuYsgIyAapAlaGlyGlyIuYsgIyAapIyGlyAlaProGIyArgProGIyArg 60  
Db 175 GGCCTCAAGAGGAGATCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234  
OY 61 ValGIyProthrgIyGlyIuYsgIyAapMerGIyAapIyGlyGlyIuYsgIySerValGIy 80  
Db 235 GTCGGCCCCACGCGGAG 294  
OY 81 ArgHISGlyIyIleGIyProIleGIySerIyGlyIuYsgIyAapSerGIyAapIle 100  
Db 295 GGTATGAGAGAAATGGTCCATTCCTTAAAGGTGAGAGAGAGAGAGAGAGAGAGAG 354  
OY 101 GlyProProGIyProAanGIyGlyIuProGIyLeuProCyGlyCySerGIyIleuArgHy 120  
Db 355 GAGACCCCTGTGCTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414  
OY 121 AlaIleGIyIuMeAapAanGlnValSerGlnleuThrSerGlnleuYspHeIleYs 140  
Db 415 GCCATCGGGGAGATGAG 474  
OY 141 AanaIaValAlaGlyValArgIuThrgIuSerIyIleYrleuIleuValIleuGlu 160  
Db 475 AATGCTGTGCGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534  
OY 161 LySaRgTyraIaAapAlaGlnleuSerCySgInGIyArgGIyGlyThrleuSerMePro 180  
Db 535 AAGCCCTACGCGGAG 594  
OY 181 LySaRgTyraIaAanGlyIleuYec 189  
Db 595 AAGGAGGAGGCTGCCAATGCGCTGATG 621

RESULT 9  
LOCUS BE382845 723 bp mRNA linear EST 21-JUN-2000  
DEFINITION 601297714F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3627794 5',  
mRNA sequence.  
ACCESSION BE382845  
VERSION BE382845.1 GI:9328210  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 723)  
AUTHORS NIH-MGC <http://mgs.mci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC

## FEATURES

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LNCM311 row: 1 column: 03  
High quality sequence stop: 632.  
Location/Qualifiers  
1..723  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3627794"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1ib="NIH\_MGC\_19"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 7.06e-171 Length: 723  
Score: 188.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 69.37% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277a-6 (1-271) x BE382845 (1-723)

OY 1 MetatrgtGlyAanleuAlaleuValGlyValleuIleSerleuAlapheluSerleu 20  
Db 55 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATACAGCTGGCTTCTGTCATGCTG 114  
OY 21 ProserGIyHISProGIInProAlaGlyAapAapAlaCySerValGlnIleleuValPro 40  
Db 115 CCATCTGACATCTCCACCGCGCTGCGCATGACGCTGCTGTGCAAGATCTCTGCTCT 174  
OY 41 GlyleuYsgIyAapAlaGlyGlyIuYsgIyAapIyGlyAlaProGIyArgProGIyArg 60  
Db 175 GGCCTCAAGAGGAGATCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234  
OY 61 ValGIyProthrgIyGlyIuYsgIyAapMerGIyAapIyGlyGlyIuYsgIySerValGIy 80  
Db 235 GTCGGCCCCACGCGGAG 294  
OY 81 ArgHISGlyIyIleGIyProIleGIySerIyGlyIuYsgIyAapSerGIyAapIle 100  
Db 295 GGTATGAGAGAAATGGTCCATTCCTTAAAGGTGAGAGAGAGAGAGAGAGAGAGAG 354  
OY 101 GlyProProGIyProAanGIyGlyIuProGIyLeuProCyGlyCySerGIyIleuArgHy 120  
Db 355 GAGACCCCTGTGCTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414  
OY 121 AlaIleGIyIuMeAapAanGlnValSerGlnleuThrSerGlnleuYspHeIleYs 140  
Db 415 GCCATCGGGGAGATGAG 474  
OY 141 AanaIaValAlaGlyValArgIuThrgIuSerIyIleYrleuIleuValIleuGlu 160  
Db 475 AATGCTGTGCGCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534  
OY 161 LySaRgTyraIaAapAlaGlnleuSerCySgInGIyArgGIyGlyThrleuSerMePro 180  
Db 535 AAGGCTACGCGGAG 594  
OY 181 LySaRgTyraIaAanGlyIleu 188







Score: 181.00 Matches: 181  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.79% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277a-6 (1-271) x BE313199 (1-683)

OY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 55 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATCAGCTGCGCTTCTGCACTGCTG 114  
OY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 115 CCATCTGGACATCTCTCAGCCGGCTGGCCAGTACGCTGCTGTCGACAAATCTCTCCCT 174  
OY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyValArgProGlyArg 60  
DB 175 GGCCTCAAGGGGATCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234  
OY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
DB 235 GTCCGCCCCACCGGAG 294  
OY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyAspSerGlyAspIle 100  
DB 295 GGTCAATGAGAAATATGCTCCATTCCTTAAAGGTGAGAAAGAGAGAGAGAGAGAGAG 354  
OY 101 GlyProProGlyProAsnGlyGlyLysProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
DB 355 GGACCCCTGTGCTCAATGAG 414  
OY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
DB 415 GCCATCGGGGAGATGAGACACAGAGCTCTCTCAGCTGACAGAGAGAGAGAGAGAGAG 474  
OY 141 AsnAlaValAlaGlyValArgGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 160  
DB 475 AATGCTGTCGCGGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534  
OY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyLysGlyThrLeuSerMetPro 180  
DB 535 AAGGCTACGCGGAG 594  
OY 181 Lys 181  
DB 595 AAG 597

RESULT 12  
BE313199 715 bp mRNA linear EST 26-OCT-2000  
LOCUS 601149012P1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3501747 5',  
DEFINITION mRNA sequence.  
BE313199  
ACCESSION BE313199.1 GI:9132817  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 715)  
NIH-MGC http://mgi.mcl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabp-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov  
Plate: LNCM172 row: h column: 04

High quality sequence stop: 643.  
FEATURES  
Location/Qualifiers  
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/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: brain; Vector: POT87; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Prod. No.: 3,71e-163 Length: 715  
Score: 180.00 Matches: 180  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.42% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277a-6 (1-271) x BE313199 (1-715)

OY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 55 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCAATCAGCTGCGCTTCTGCACTGCTG 114  
OY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 115 CCATCTGGACATCTCTCAGCCGGCTGGCCAGTACCGCTGCTGTGACAAATCTCTCCCT 174  
OY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyValArgProGlyArg 60  
DB 175 GGCCTCAAGGGGATCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234  
OY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80  
DB 235 GTCCGCCCCACCGGAG 294  
OY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyGlyLysGlyLysGlyLysGlyLys 100  
DB 295 GGTCAATGAGAAATATGCTCCATTCCTTAAAGGTGAGAAAGAGAGAGAGAGAGAGAG 354  
OY 101 GlyProProGlyProAsnGlyGlyLysProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
DB 355 GGACCCCTGTGCTCAATGAG 414  
OY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
DB 415 GCCATCGGGGAGATGAGACACAGAGCTCTCTCAGCTGACAGAGAGAGAGAGAGAGAG 474  
OY 141 AsnAlaValAlaGlyValArgGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 160  
DB 475 AATGCTGTCGCGGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534  
OY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyLysGlyThrLeuSerMetPro 180  
DB 535 AAGGCTACGCGGAG 594

RESULT 13  
BF312666 613 bp mRNA linear EST 21-NOV-2000  
LOCUS BF312666  
DEFINITION 601898164P1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4127486 5',  
ACCESSION mRNA sequence.  
BF312666  
VERSION BF312666.1 GI:11260511

**KEYWORDS**  
EST.

**SOURCE**  
Homo sapiens (human)

**ORGANISM**  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE**  
1 (bases 1 to 613)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)

**AUTHORS**  
Contact: Robert Strausberg, Ph.D.  
Email: cgsabbs-rc@mail.nih.gov  
Tissue Procurement: ATCC

**JOURNAL**  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: [image.lnl.gov](http://image.lnl.gov)  
Plate: LILCM018 row: P column: 15  
High quality sequence stop: 612.  
Location/Qualifiers  
1..613

**FEATURES**  
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/note="Organ: brain; Vector: pORF7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGGCAGG(G). Library constructed by Ling Hong  
in the laboratory of Gerald W. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

**ALIGNMENT SCORES:**

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-09-806-277A-6 (1-271) x BF312666 (1-613)	2,966-162	179.00	100.00%	66.05%	2
	Length:	Matches:	Conservative:	Mismatches:	Gaps:
	613	179	0	0	0

**ORIGIN**

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

Db		435	GCCATCGGGAGATGACCAACCAGGTCTCTCAGCTGACCAACGAGCTCAAGTTCAATCAAG	494
Oy		141	AAsplalaValaIagIyValaYargIuThnglUsertVsiIeTyrlEuleuVallysgIuglu	160
Db		495	AATCTCTTCGCCGGTGTGC GGGAACGAGACCAAGATCTACTCTGTGTGAAGAAGANG	554
Oy		161	LysArGTyAlaAapalaginLseuSerCyaglInglYargIyglYThLeuSerMet	179
Db		555	AAGGCTAACGGGAGCGCCAGCTGTCTCTGACGAGGCGCGGGGGGACAGCTGAGCATG	611
RESULT 14				
LOCUS	BE312923			
DEFINITION	601146744F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161914 5'	654 bp	mRNA	linear EST 26-OCT-2000
ACCESSION	BE312923			
VERSION	BE312923.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ 1 (bases 1 to 654) National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabds@email.nih.gov Tissue Procurement: ATCC			
AUTHORS	CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov Plate: LICM120 row: h column: 11 High quality sequence stop: 590.			
JOURNAL				
COMMENT				
FEATURES				
source				
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	1..654			
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	/clone_lib="NIH_MGC_19"			
	/note="Organ: Brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC Library."			
ORIGIN				
Alignment Scores:				
Pred. NO.:	2,29e-158	Length:	654	
Score:	175.00	Matches:	175	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatch:	0	
Query Match:	64.58%	Indels:	0	
	2	Gaps:	0	
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Oy		1	MeArGgIyAnLnuAlaLeuValGlYValleuIleSerIeuAlaPheluSerIeuLen	20
Db		55	ATGAGGGGGAATCTGGCCCTGCTGGCGCTTTAAACACCTGGCGCTTCTGTGCACGTG	114
Oy		21	ProGerGIyHSPrOGInPrioAlaGlYAspaApalaCYSeSerVaIGlnIleLeuValPro	40
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Qy 41 GlyLeuYsgLYaAPaLAgLYGluYsgLYaAPLYsgLYaLAProGLYArgProGLYArg 60
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Db 235 GTGGCCCGGAGGAGAAAGAGACATGGGGGCAAAAGACAGAAAGGCAAGTGTGGGT 294
Qy 81 ArgHsGLYLYsGLYsGLYProLLeGLYsGLYsGLYsGLYsGLYsGLYsGLYsGLYsGLYs 100
Db 295 CGTATGGAATAATTGCTCCATTCCTTAAGGTGAGAAAGAGATTCCGGTACATA 354
Qy 101 GlyProProGLYProaENGlyGluProGLYLeuProCYsGLYCySseGLInLeuArgLYs 120
Db 355 GGACCCCTGCTCTTAATGAGAACAGCCCTCCATGTGATGACGACGCGGCAAG 414
Qy 121 AlaLLeGLYGLMeAPaAngGLNValSerGLInLeuThrSerGLInLeuLYsPheLLeLYs 140
Db 415 GCCATCGGGAGATGACACACAGGTCTCTCAGCTGACAGGAGCTCAAGTTCTCAAG 474
Qy 141 AsnAlaValAlaGLYValArgGLuThrGLuSerLYsLLeTYrLeuLeuValLYsGLuGLu 160
Db 475 AATGCTGCGCGGTGTGCGGAGACGGAAGCAAGATCTACCTGCTGTGAAGAGAGAG 534
Qy 161 LysArgTYrAlaAPaLAgLYGlnLeuSerCYsGLInLYaArgLYGly 175
Db 535 AAGCGCTACGGGAGACGCGGCTGTCTGCCAGCGCGGCGGCGG 579

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## RESULT 15

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LOCUS BE260904 1012 bp mRNA linear EST 26-OCT-2000
DEFINITION 601153812P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509811 5',
RNA sequence.
ACCESSION BE260904
VERSION BE260904.1 GI:9132588
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1012)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rmail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L16M193 row: h column: 04
High quality sequence stop: 615.
Location/Qualifiers
1..1012
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_image="3509811"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

```

## FEATURES

## SOURCE

ORIGIN

```

Alignment Scores:
Pred. No.: 3,45e-158 Length: 1012
Score: 175.00 Matches: 175
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.58% Indels: 0
DB: 2 Gaps: 0

```

US-09-806-277A-6 (1-271) x BE260904 (1-1012)

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Qy 1 MeArGgLYaenLeuAlaLeuValGLYValLeuLLeSerLeuAlaPheLeuSerLeu 20
Db 56 ATGAGGGGGAATCTGGCCCTGTGGGCTTCTAATCAGCTTGCCCTTCTCTGCTG 115
Qy 21 ProSerGLYHsProGLInProALaGLYAspAPaLAcYsSerValGLInLeuValPro 40
Db 116 CCATCTGGACATCTCTCAGCCGCGGTGGCGATACGCTGTGTGACATCTCTGCTCCT 175
Qy 41 GlyLeuYsgLYaAPaLAgLYGluYsgLYaAPLYsgLYaLAProGLYArgProGLYArg 60
Db 176 GGCTCAAAAGGGAGATGCGGAGAGAGAGAGCAAAAGCGCCCGGACGGCTTGAAAGA 235
Qy 61 ValGlyProThrGlyGluYsgLYaAPMeTgLYaAPLYsgLYGlnLYaGlySerValGly 80
Db 236 GTGGCCCGGAGGAGAAAGAGACATGGGGGCAAAAGGACAGAAAGGCAAGTGTGGGT 295
Qy 81 ArgHsGLYLYsGLYsGLYProLLeGLYsGLYsGLYsGLYsGLYsGLYsGLYsGLYsGLYs 100
Db 296 CGTATGGAATAATTGCTCCATTCCTTAAGGTGAGAAAGAGATTCCGGTACATA 355
Qy 101 GlyProProGLYProaENGlyGluProGLYLeuProCYsGLYCySseGLInLeuArgLYs 120
Db 356 GGACCCCTGCTCTTAATGAGAACAGCCCTCCATGTGATGACGACGCGGCAAG 415
Qy 121 AlaLLeGLYGLMeAPaAngGLNValSerGLInLeuThrSerGLInLeuLYsPheLLeLYs 140
Db 416 GCCATCGGGAGATGACACACAGGTCTCTCAGCTGACAGGAGCTCAAGTTCTCAAG 475
Qy 141 AsnAlaValAlaGLYValArgGLuThrGLuSerLYsLLeTYrLeuLeuValLYsGLuGLu 160
Db 476 AATGCTGCGCGGTGTGCGGAGACGGAAGCAAGATCTACCTGCTGTGAAGAGAGAG 535
Qy 161 LysArgTYrAlaAPaLAgLYGlnLeuSerCYsGLInLYaArgLYGly 175
Db 536 AAGCGCTACGGGAGACGCGGCTGTCTGCCAGCGCGGCGGCGG 580

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Search completed: December 17, 2004, 14:19:52  
 Job time : 3871 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 10:04:40 ; Search time 5448 Seconds  
(without alignments)  
2352.333 Million cell updates/sec

Title: US-09-806-277A-6

Sequence: 1 MRGNLALVGLISLAFSL.....NDVACHTTMTMCEFDXNM 271

## Scoring table:

OLIGO  
Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9045947

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

## Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool.p/US09806277/runat.15122004.101700.29752/app.query.fasta.1.455  
-DB=genembl -OEMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09806277@CGN 1.1 7406@runat.15122004.101700.29752 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

## Database :

Genembl: 1: gb.ba:\*  
2: gb.hcg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.scs:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	271	100.0	813	6	BD103332 Novel col
2	271	100.0	1238	6	AR252616 Sequence
3	271	100.0	1238	6	AX403469 Sequence
4	271	100.0	1238	6	AX454582 Sequence

5	271	100.0	1238	6	AX491060
6	271	100.0	1238	9	AY358439
7	271	100.0	1248	9	BC000078 Homo sapi
8	271	100.0	1341	6	BD103302 Novel col
9	228	84.1	735	6	BD103333
10	228	84.1	1139	6	BD103303 Novel col
11	205	75.6	741	6	BD103340 Novel col
12	205	75.6	1269	6	BD103330
13	204	75.3	663	6	BD103336
14	204	75.3	1067	6	BD103305
15	204	75.3	1417	6	BC009951
16	181	66.8	663	6	BD103337
17	181	66.8	669	6	BD103339
18	181	66.8	741	6	BD103341
19	181	66.8	1067	6	BD103306
20	181	66.8	1197	6	BD103329
21	180	66.8	1269	6	BD103331
22	180	66.4	591	6	BD103335
23	180	66.4	995	6	BD103304
24	159	58.7	477	6	BD103334
25	142	52.4	708	6	CQ716215
26	130	48.0	139357	9	AC010907 Homo sapi
27	49	18.1	246539	2	AC125638
28	47	17.3	813	6	BD103338
29	47	17.3	1522	6	BD103307
30	34	12.5	175475	2	AC123631
31	25	9.2	648	11	EV075463
32	25	9.2	175475	2	AC123631
33	18	6.6	1272	5	BC056052
34	17	6.3	231062	2	AC109110
35	16	5.9	612	6	BD103308
36	15	5.5	979	5	CR338949 Gallus ga
37	15	5.2	206332	10	AC136986
38	12	4.4	212049	5	EX005484
39	12	4.4	229319	2	CR354585
40	11	4.1	89	6	AX920471
41	11	4.1	89	6	BD056004
42	11	4.1	2721	3	SC4572
43	11	4.1	6006	3	SUSCOP
44	10	3.7	93	6	AR074458
45	10	3.7	93	6	AR081138

## ALIGNMENTS

RESULT 1	BD103332	813 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD103332				
DEFINITION	Novel collectin.				
ACCESSION	BD103332				
VERSION	BD103332.1				
KEYWORDS	WO 0181401-A/31.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Wakamiya, N., Keshi, H., Otani, K., Sakamoto, T. and Kishi, Y.				
TITLE	Novel collectin				
JOURNAL	Patent: WO 0181401-A 31 01-NOV-2001; FUSO PHARMACEUTICAL INDUSTRIES LTD, NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI				
COMMENT	OS Homo sapiens (human) PN WO 0181401-A/31 PD 01-NOV-2001 PF 23-APR-2001 WO 2001JP003468 PR 21-APR-2000 JP 00P 120358 PI NOBUTAKA WAKAMIYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI PI YUICHIRO KISHI PC C07K14/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53 CC Novel collectin FH key Location/Qualifiers				

[illegible]

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LOCUS	AR252616	1238 bp	DNA
DEFINITION	Sequence 356 from patent US 6478825.		linear
ACCESSION	AR252616		PAT 20-DEC-2002
VERSION	AR252616.1	GI:27300524	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1238)		
TITLE	Wintebottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.		
JOURNAL	Implant, method of making same and use of the implant for the		
FEATURES	treatment of bone defects		
source	Patent: US 6478825-A 356 12-NOV-2002;		
	Location/Qualifiers		
	1..1238		
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ORIGIN			
Alignment Scores:			
Pred. No.:	1,45e-262	Length:	1238
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Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-806-277A-6 (1-271) x AR252616 (1-1238)			
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QY	21	ProSerGlyYhiSPROGInPtoAlaGlyAaSPaAlaCySerValGlnIleleuValPro	40
Db	127	CCATCTGGACATCTCTCAGCCGGCTGGAGTAGCGCTCTGTGCGAGATCTGTCTCT	186
QY	41	GlyleuIySgIyAaPaAlaGlyGlyIuIySgIyAaSPaIyAlaProGlyYATProGlyYArg	60
Db	187	GGCTTCAAAGGGATGCGGAGAGAAAGGACAAAGGCGCCCCGAGCGCTCGAAGA	246
QY	61	ValGlyProThrgIyGlyIuIySgIyAaSPaGlyAaSPaIyGlyIuIySgIySerValGly	80
Db	247	GTCGGCCCCAGGGAGAAAGGAGACATGGGGACAAAGACAGAAAGGACAGTGGGT	306
QY	81	ArgHtgIyYhiIleGlyProIleGlySerIyGlyGlyIuIySgIyAaSPaIyAaSPaIle	100
Db	307	CGTATGAGAAATATGTGTCCATTTGGTCTPAAGAGTAGAAGAGAGATTCCGTGACATA	366
QY	101	GlyProProGlyProAaenGlyGlyIuProGlyIleuProCySgIuCySgSerGInleuArgIys	120
Db	367	GGACCCCTGCTCTTATGAGAAACAGGGCTCCCATGATGAGAGACAGCTGCGCAG	426
QY	121	AlaIleGlyIuIeIuIeAaPaenGInValSerGInleuThrsGInleuIySpheIeIys	140
Db	427	GCCATCCGGGAGAGGCAACACAGGTCTCTCAGCTGACACAGCAGGCTCAAGTTCATCAG	486
QY	141	AaPaAlaValAlaGlyValaArgGlyIuThGInIuSerIyIleIyIleIuIeValIySgIuIu	160
Db	487	AATCTGTGCGCGGTGTGCGGAGACGAGACGAGAACAGATCTTACCTGCTGTGTAAGAGAGAG	546
QY	161	LysArgTyrAlaAaPaIaGInleuSerCySgInGlyArgGlyGlyIuIyThrsIeuSerMetPro	180
Db	547	AAGGCTAACCGGAGCGCCAGCTGTCTGTCCAGGGCGCGGGGGCAGCTGAGATGCC	606
QY	181	LysAaSPaIuIaIaAaenGlyIeMetAlaAlaIyIleuAlaGInAlaGlyIleuAlaArg	200
Db	607	AAGACAGAGGCTGCAATGAGCTGTATGGCCGACATCTTGGCGCAAGCGGAGCTGGCCGT	666

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Qy 221 PrometArgThrPheAsnLysTrpArgSerGlyGluProAsnAsnAlaTyrAspGlu 240  
Db 727 CCATCGGGGACCTTCAACAGATGGGCGACGGGTGAGCCCAACATGCTTACAGAGAG 786  
Qy 241 AspCysValAlaMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrMet 260  
Db 787 GACTGCGTGAGATGGTGGCTCGGGCGGCTGGAACGACGTGGCTGCACACCACTAG 846  
Qy 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 847 TACTTCATGTGTGAGTTGACAGAGAACATG 879

RESULT 3  
AX403469 1238 bp DNA linear PAT 14-JUN-2002  
LOCUS Sequence 356 from Patent WO0073454.  
DEFINITION AX403469  
VERSION AX403469.1 GI:21436970  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1  
Ferrara N., Gerber H., Gerritsen M., Goddard A., Godowski P.,  
Grimaldi C.J., Gurney A.L., Kijavlin I., Napier M.A., Pan J.,  
Paoni N.F., Roy M., Stewart T.A., Tumas D., Watanabe C.K.,  
Williams P., Wood W.I. and Zhang Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0073454-A 356 07-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
SOURCE Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Alignment Scores:  
Pred. No.: 1.45e-262 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-806-277A-6 (1-271) x AX403469 (1-1238)

Qy 101 GlyProGlyProAsnGlyGluProGlyLeuProCysGlyCysSerGlnLeuArgLys 120  
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Qy 121 AlaIleGlyIleMetAspAsnGlnValSerGlnLeuThrSerGluLeuLysPheLys 140  
Db 427 GCCATCGGGAGATGACACACAGTCTCTAGCTGACAGCGAGCTCAATTCATCAAG 486  
Qy 141 AsnAlaValAlaGlyValArgGlyThrGluSerLysIleTyrLeuLeuValGlyGlu 160  
Db 487 AATCTGTGGCGGTGTGCGCGAGACGAGCAAGATCTACCTGCTGTGAAGAGAG 546  
Qy 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnIleTyrArgGlyTyrThrLeuSerMetPro 180  
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Db 667 GTCTTCATGGCATCAACGACCTGGAGAGAGGGCGCTTCGTGACTGACCACTCC 726  
Qy 221 PrometArgThrPheAsnLysTrpArgSerGlyGluProAsnAsnAlaTyrAspGlu 240  
Db 727 CCATCGGGGACCTTCAACAGATGGGCGACGGGTGAGCCCAACATGCTTACAGAGAG 786  
Qy 241 AspCysValAlaMetValAlaSerGlyGlyTyrPheAspValAlaCysHisThrMet 260  
Db 787 GACTGCGTGAGATGGTGGCTCGGGCGGCTGGAACGACGTGGCTGCACACCACTAG 846  
Qy 261 TyrPheMetCysGluPheAspLysGluAsnMet 271  
Db 847 TACTTCATGTGTGAGTTGACAGAGAACATG 879

RESULT 4  
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LOCUS Sequence 167 from Patent WO0208284.  
DEFINITION AX454582  
VERSION AX454582.1 GI:21713915  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1  
Baker K.P., Ferrara N., Gerber H., Gerritsen M.E., Goddard A.,  
Godowski P.J., Gurney A.L., Hillan K.J., Hirst S.A., Pan J.,  
Paoni N.F., Stephan J.P., Watanabe C.K., Williams P.M., Wood W.I.  
and Ye W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 167 31-JUN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Hirst, Scott A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Alignment Scores:  
Pred. No.: 1.45e-262 Length: 1238  
Score: 271.00 Matches: 271

Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 Gaps: 0  
 Indels: 0  
 Mismatches: 0

US-09-806-277a-6 (1-271) x AK454582 (1-1238)

QY 1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20  
 Db 67 ATGAGGGGGAATCTGGCCCTGCTGCTTCTAATCAAGCCCTGCTTCTCACTCTG 126  
 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACGCTGCTGTGGAGATCTTGTCTCCT 186  
 QY 41 GlyLeuysGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 60  
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 QY 61 ValGlyProThrGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
 Db 247 GTCGGCCCAAG 306  
 QY 81 ArgHisGlyValIleGlyProIleGlySerValGlyValGlyValGlyValGlyValGly 100  
 Db 307 CGTATGGAGAAATTTGCTCCATTTGCTCTTAAGGCTGAGAGAGAGAGAGAGAGAGAT 366  
 QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyCysSerGlnLeuValGly 120  
 Db 367 GAGACCCCTGCTCTAATGAG 426  
 QY 121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlyValGlyValGlyVal 140  
 Db 427 GCGATCGGGAG 486  
 QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
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 QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValGlyValGlyValGlyValGly 180  
 Db 547 AAGGCTAAGCGGAG 606  
 QY 181 LysAspGlyValAlaAsnGlyValMetAlaAlaTyrLeuAlaGlnAlaGlyValLeuAla 200  
 Db 607 AAGAGCGAGGCTGCAATGCTATGCGCCCAATGCTGCGAGAGAGAGAGAGAGAGAGAG 666  
 QY 201 ValPheIleGlyIleAsnAspLeuGlyValGlyValGlyValGlyValGlyValGlyVal 220  
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 QY 221 ProMetArgThrPheAsnGlyTyrPargSerGlyValProAsnAlaAlaTyrAspGly 240  
 Db 727 CCCATGCGGAG 786  
 QY 241 AspCysValGlyMetValAlaSerGlyValTyrPheAspAlaAlaCysHisThrThrMet 260  
 Db 787 GACTGCTGAG 846  
 QY 261 TyrPheMetCysGlyValPheAspGlyValGlyValGlyValGlyValGlyValGly 271  
 Db 847 TACTTCAATGCTGAG 879

RESULT 5  
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 DEFINITION Sequence 167 from Patent WO0200690.  
 ACCESSION AX491060  
 VERSION AX491060.1 GI:22323867  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
 Pao, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
 and Ye, W.

## TITLE

Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0200690-A 167 03-JAN-2002;

Genentech, Inc. (US)

## FEATURES

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## ORIGIN

## Alignment Scores:

Pred. No.: 1,45e-262 Length: 1238  
 Score: 271.00 Matches: 271  
 Percent Similarity: 100.00% Conserved: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-806-277a-6 (1-271) x AK491060 (1-1238)

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 QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
 Db 127 CCATCTGGACATCTCTCAAGCCGCTGGCGATGACGCTGCTGTGGAGATCTTGTCTCCT 186  
 QY 41 GlyLeuysGlyAspAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 60  
 Db 187 GGCCTCAAGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
 QY 61 ValGlyProThrGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 80  
 Db 187 GGCCTCAAGAGGAGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
 QY 81 ArgHisGlyValIleGlyProIleGlySerValGlyValGlyValGlyValGlyValGly 100  
 Db 247 GTCGGCCCAAG 306  
 QY 101 GlyProProGlyProAsnGlyGlyProGlyLeuProCysGlyCysSerGlnLeuValGly 120  
 Db 367 GAGACCCCTGCTCTAATGAG 426  
 QY 121 AlaIleGlyGlyMetAspAsnGlnValSerGlnLeuThrSerGlyValGlyValGlyVal 140  
 Db 427 GCGATCGGGAG 486  
 QY 141 AsnAlaValAlaGlyValAlaGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
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 QY 181 LysAspGlyValAlaAsnGlyValMetAlaAlaTyrLeuAlaGlnAlaGlyValLeuAla 200  
 Db 607 AAGAGCGAGGCTGCAATGCTATGCGCCCAATGCTGCGAGAGAGAGAGAGAGAGAGAG 666  
 QY 201 ValPheIleGlyIleAsnAspLeuGlyValGlyValGlyValGlyValGlyValGlyVal 220  
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 QY 221 ProMetArgThrPheAsnGlyTyrPargSerGlyValProAsnAlaAlaTyrAspGly 240



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Db      727  CCATGCGGACCTTCAACAGATGGGCGACGGGTGAGCCCAACATGCTTACGACGAGAG 786
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Db      787  GACTCGGTGAGATGTGGCTCTCGGGCGGCTGGAACGACGTGGCTGCACACCAACATG 846
Qy      261  TyrPheMetCyvGluPheAspGlyGluAsnMet 271
Db      847  TACTTCATGTGTGAGTTTGACAAAGAGAACATG 879

RESULT 6
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DEFINITION Homo sapiens clone DNAS59848 RGNL596 (UNQ596) mRNA, complete cds.
VERSION  AY358439.1 GI:37182002
KEYWORDS  FLI CDNA.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Curral,C., Gu,Q., Hase,P.E.,
Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robble,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagte,A., Vandlen,R., Watanabe,C., Wiand,D., Woods,K.,
Xie,M.H., Yanura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL  PUBMED
REFERENCE 12975309
AUTHORS  Clark,H.F.
TITLE     Direct Submision
JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES  Location/Qualifiers
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ORIGIN
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Pred. No.:      1,456-262      Length:      1238
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Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:    100.00%         Indels:      0
Gaps:           9              0

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Db      127  CCATCTGGAACATCTCTCAGCCGGCTGGCGATACGCTCTCTGTGCAATCTCTGCTCCCT 186
Qy      41  GlyLeuIleGlyAspAlaGlyGlyLeuGlyAspGlyGlyAlaProGlyArgProGlyArg 60
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Qy      81  ArgHisGlyLeuIleGlyProIleGlySerIleGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db      307  CGTATGAGAAAAATTGCTCCATTTGCTTAAAGGTGAGAAAGAGAGATTCCGGTGACATA 366
Qy      101  GlyProProGlyProAsnGlyGlyProGlyLeuProGlyGlyGlyGlyGlyGlyGlyGly 120
Db      367  GGACCCCTGGTCTTAATGAGAGAACAGGCTCCCATGTGATGACGACCTGCGCAAG 426
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Qy      181  LysAspGlyAlaAlaAsnGlyLeuMetAlaIleThrLeuAlaGlnAlaGlyLeuAlaArg 200
Db      607  AAGAGCGAGGCTGCAATGAGCTGTGAGCCCATACCTCGGAGCAAGCGGAGCTGAGCCGT 666
Qy      201  ValPheIleGlyIleAsnAspLeuGlyGlyGlyGlyAlaPheValTyrSerAspHisSer 220
Db      667  GTCTTCATCGGCATCAACAGACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
Qy      221  ProMetArgThrPheAsnLeuTyrArgSerGlyGlyProAsnAsnAlaTyrAspGlyGly 240
Db      727  CCATGCGGACCTTCAACAGATGGGCGACGGGTGAGCCCAACATGCTTACGACGAGAG 786
Qy      241  AapCyvValGluMetValAlaSerGlyGlyTTPaanaapValAlaCyvHisThrThrMet 260
Db      787  GACTCGGTGAGATGTGGCTCTCGGGCGGCTGGAACGACGTGGCTGCACACCAACATG 846
Qy      261  TyrPheMetCyvGluPheAspGlyGluAsnMet 271
Db      847  TACTTCATGTGTGAGTTTGACAAAGAGAACATG 879

RESULT 7
LOCUS   BC000078                1248 bp    mRNA    linear    PRI 30-JUN-2004
DEFINITION Homo sapiens collectin sub-family member 11, transcript variant 1,
mRNA (cdna clone MGC:3279 IMAGF:3507377), complete cds.
ACCESSION BC000078.2 GI:33990875
VERSION    BC000078.2
KEYWORDS   MGC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Strausberg,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stuplet, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Uedl, T.B., Toshiyuki, S., Cantucci, P., Prange, C., Raha, S.S., Loggiano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Boeck, S.A., McEwen, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Woreley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalhus, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
2 (bases 1 to 1248)

Strauberg, R.  
Direct Submission  
Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 20, 2003 this sequence version replaced gi:12652660.  
Contact: MGC help desk  
Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed By: The I.M.A.G.E. Consortium (ILMIL)  
DNA Sequencing By: Institute for Systems Biology  
<http://www.systemsbio.org>  
Contact: [amadane@systemsbio.org](mailto:amadane@systemsbio.org)  
Amp Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: <http://image.llnl.gov>  
Series: IRL Plate: 7 Row: 9 Column: 20  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13128971.

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Location/Qualifiers  
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DB: 9 Gaps: 0

US-09-806-277A-6 (1-271) x BC000078 (1-1248)

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Db 134 CCACTCGACATCTCAGCGCGCTGGGAGATGACGCTGCTGAGATCTCTGCTCCT 193

QY 41 GlyLeuLysGlyAspAlaGlyLysGlyAspLysGlyValAlaProGlyArgProGlyArg 60  
Db 194 GGCCTCAAGGGAGATCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 253

QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyValLysGlySerValGly 80  
Db 254 GTGCGGCCCAAGGAG 313

QY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyValLysGlyAspSerGlyAspIle 100  
Db 314 CGTATGAGAAATATGATCCATTCCTTAAGTGTAGAGAGAGAGAGAGAGAGAG 373

QY 101 GlyProProGlyProAsnGlyLysProGlyLysProCysGlyLysSerGlnLeuArgLys 120  
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QY 121 AlaIleGlyLysMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLysPheIleLys 140  
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QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyValGlyLysThrLeuSerMetPro 180  
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QY 181 LysAspGlnAlaAlaAsnGlyLysMetAlaAlaTyrLeuAlaGlnAlaLysAlaArg 200  
Db 614 AAGGACGAGGCTGCAATGCTGATGCGCATTACTGCGCAAGCGGCTGCGCCGT 673

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QY 221 ProMetArgThrPheAsnLysTyrPAspSerGlyGlnProAsnAsnAlaTyrAspGluGlu 240  
Db 734 CCATGCGGACCTTCAACAGAGTGGCGAGCGGAGAGAGAGAGAGAGAGAGAGAG 793

QY 241 AspCysValGlnMetValAlaSerGlyGlyTyrAsnAspValAlaCysHisThrThrMet 260  
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RESULT 8  
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LOCUS Novel collectin.  
DEFINITION BD103302  
ACCESSION BD103302.1 GI:22648876  
VERSION  
KEYWORDS WD 0181401-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.  
1 (bases 1 to 1341)  
Wakamaya, N., Keshi, H., Ocani, K., Sakamoto, T. and Kishi, Y.  
Novel collection  
Patent: WO 0181401-A 1 01-NOV-2001;  
JOURNAL

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Best Local Similarity:	100.00%
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	Gaps: 0
US-09-806-277A-6 (1-271) x BD103302 (1-1341)	
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Best Local Similarity:	100.00%	Mismatches:	0
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DB:	6	Gaps:	0
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DB	192	GGGATGGGGAGAGAAAGGAGACAAAGGCCCGCCCCCGCCTGGAGAAGTGGCCCC	251
QY	64	ThxGIYLUYSGLYAEPMeGILYAEPYASGLYLVSGLYSERVALGIYARHIGLY	83
DB	252	ACGGAGAAAAAGAGACATGGGGGCACAAGAGACAGAAAGCATGTGGTGTCATGGA	311
QY	84	LysLIEGLYProLIEGLYSERLYSGLYLVLVSGILYAPSPERGILYAEPILEGYProPro	103
DB	312	AAAATGTGCTCCATTGCTCTTAAGGTGAGAAAGAAATTCCTGGTGCAATGGACCCCCT	371
QY	104	GIYProABNGIYGIUPROGILYLEUPROCYSGILUCYSERGINLEUAATGLYSAIAILEGLY	123
DB	372	GGTCTTAATGAGAACCAAGGCTCCATGTGATGTGACGACGCTGGCCAAGGCATCGGG	431
QY	124	GIUMETASPENGINVALISERGINLEUTHSERGILULEULYSPHEILEYBARNALVAL	143
DB	432	GAGATGAGAACACCGGCTCTCACCTACCAAGCAAGCTCAAGTTCAATCAAGATGCTGC	491
QY	144	ALAgiYVALARgGiUTNrGILUSerLYIIETyrLEuleuVALlySGiUGILUYARgTYr	163
DB	492	GCCCGTGTGCCGAGACGAGAGCAAAATCTACTGCTGTGTGAAGAGAGAAAGCGCTAC	551
QY	164	AlAapLAagInLeuSerCyrgingLYARgLYGIYThrLeuSerMetProLYASPGILU	183
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QY	184	AlAalAaenGIyLeuMetAlAaLYTyrrLeuAlAGlnlAGLyLeuAlAARgVALPheILE	203
DB	612	GCTGCATAATGCCGATAGCCGCAATACCCTGGCGCAAGCGGCTGGCCGCTGTTTATC	671
QY	204	GIYLIeAnApLeuGIULYSGILUIYALPheVALYrSerAAPHIsErPrometArG	223
DB	672	GGCATCAACGACCTGGAGAAAGAGAGGCGCTTGTAATCTGACCACTCCCCATGGGG	731
QY	224	ThrPheasnLYrTPRAsgerGILYGIUProABNArnAlAYrAPrGILUGILYAsPCyVal	243
DB	732	ACCTTCAAACAAGTGGCCAGCGGTGAGACCCCAACATATCTPAACGAGAGAGATGGGTG	791
QY	244	GIUmEtVALIASerGIYGLYTrPAsnAspVALAACYshIsrThrmEctYrPhEmet	263
DB	792	GAGATGTGTGGCTGGGGCGCTGGAAAGACGTGGCTTGCCACACCAATGTAATCTCATG	851
QY	264	CysGIUpHeapPLYSGILUAsnMet	271
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DEFINITION	Novel collectin.		
ACCESSION	BD103340		
VERSION	BD103340.1 GI:22648914		
KEYWORDS	WO 0181401-A/39.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE 1 (bases 1 to 741)  
AUTHORS Makamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Patent: WO 0181401-A 39 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA MAKAMIYA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/39  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA MAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
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US-09-806-277A-6 (1-271) x BD103340 (1-741)

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DB 187 CCCATTGGCTCTAAAGGTGAAGAAAGAAATTCGGTGAATAGAGACCCCTGGTCTTAT 246  
QY 107 GlyLysProGlyLysLeuProCysGlnCysSerGlnLeuArgLysAlaIleGlyGluMetAsp 126  
DB 247 GGAAGAACCAAGGCTCTCCATGTGAGTGCAGCCAGCTGCCCAAGGCCATCGGGGAGATGAC 306  
QY 127 AenglnValSerGlnLeuThrSerGlnLeuLysPheIleLysAsnAlaValAlaGlyVal 146  
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QY 147 ArgGluThrGlnSerLysIleTyrLeuLeuValLysGluGluLysArgTyrAlaAspAla 166  
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QY 167 GlnLeuSerCysGlnGlyArgGlyLysThrLeuSerMetProLysAspGluAlaAlaAsn 186  
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QY 187 GlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArgValPheIleGlyTyrLeu 206  
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QY 207 AspleuGluLysGluGlyAlaPheValTyrSerAspHisSerProMetArgThrPheAsn 226  
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QY 267 AspleysGluAsnMet 271  
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DEFINITION Novel collection.  
ACCESSION BD103330  
VERSION BD103330.1 GI:22648904  
KEYWORDS WO 0181401-A/29.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1269)  
AUTHORS Makamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.  
TITLE Novel collection  
JOURNAL Patent: WO 0181401-A 29 01-NOV-2001;  
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA MAKAMIYA,HIROYUKI  
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI  
COMMENT OS Homo sapiens (human)  
PN WO 0181401-A/29  
PD 01-NOV-2001  
PF 23-APR-2001 WO 2001JP003468  
PR 21-APR-2000 JP 00P 120358  
PI NOBUTAKA MAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI  
SAKAMOTO,  
PI YUICHIRO KISHI  
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53  
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FH Key Location/Qualifiers  
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Query Match: 75.65% Indels: 0  
DB: Gaps: 0

US-09-806-277A-6 (1-271) x BD103330 (1-1269)

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QY 87 ProIleGlySerLysGlyGluLysGlyAspSerGlyAspIleGlyProProGlyProAsn 106  
DB 451 CCCATTGGCTCTAAAGGTGAAGAAAGAAATTCGGTGAATAGAGACCCCTGGTCTTAT 510  
QY 107 GlyLysProGlyLysLeuProCysGlnCysSerGlnLeuArgLysAlaIleGlyGluMetAsp 126  
DB 511 GGAAGAACCAAGGCTCTCCATGTGAGTGCAGCAGCTGCCCAAGGCCATCGGGGAGATGAC 570  
QY 127 AenglnValSerGlnLeuThrSerGlnLeuLysPheIleLysAsnAlaValAlaGlyVal 146  
DB 571 AACCAAGTCTCTCAGACTGACCAAGCTCAAGTTCAATCAAGAAATGCTGCGCGGTGTG 630  
QY 147 ArgGluThrGlnSerLysIleTyrLeuLeuValLysGluGluLysArgTyrAlaAspAla 166  
DB 631 CGCGAGACGAGACCAATCTACCTGCTGTGAAGAGAGAAAGCGCTACGCGAGCC 690

QY	167	glnLeuSerCysGlnGlyValArgGlyValYthrLeuSerMetProTyrAspGlyValAlaIAsn	186
Db	691	CAGCTGTCCTCCACGAGCGCCGGGGGACCGCTGAGCAATGCCCAAGAGAGAGCTGCCAAT	750
QY	187	GlyLeuMetAlaAlaTyrLeuValGlnAlaGlyLeuAlaArgValPheIleGlyTLeuAsn	206
Db	751	GGCTGATAGCGCGCATACCTGAGCGAACCAGCCGCGCTGATCTTCATCGAGCATCAAC	810
QY	207	AspLeuGlyIuylArgGlyValAlaPheValTyrSerAspHisSerProMetArgThrPheAsn	226
Db	811	GACCTGGAGAAAGAGAGGGCGCTTCGTGTACTCTTGACCACTCCCATCGAGACTTCAAC	870
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Db	871	AAAGTGGCCCAACCGGTGAGACCCCAACAATCCCTACGACGAGAGAGACTGCTGAGAGATGGTG	930
QY	247	AlaSerGlyGlyTyrTrpAsnAspValAlaCysHisThrThrMetTyrPheMetCysGluPhe	266
Db	931	GCCTCGGCGGCGCTGGAAAGAGCTGAGCTGCACACCAACCATGTACTTATGTATGTATGTTT	990
QY	267	AspIlySerGluAsnMet	271
Db	991	GACAAAGAGAACATCG	1005
RESULT 13			
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LOCUS	BD103336	663 bp	DNA linear PAT 27-AUG-2002
DEFINITION	Novel collectn.		
ACCESSION	BD103336		
VERSION	BD103336.1 GI:22648910		
KEYWORDS	WO 0181401-A/35.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 663)		
AUTHORS	Wakamaya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.		
TITLE	Novel collectn		
JOURNAL	Patent: WO 0181401-A 35 01-NOV-2001; FUSO PHARMACEUTICAL, INDUSTRIES LTD, NOBUTAKA WAKAMAYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI SAKAMOTO, YUICHIRO KISHI		
COMMENT	OS Homo sapiens (human) PN WO 0181401-A/35 PD 01-NOV-2001 PF 23-APR-2001 WO 2001JP003468 PR 21-APR-2000 JP 00P 120358 PI NOBUTAKA WAKAMAYA, HIROYUKI KESHI, KATSUKI OTANI, TAKASHI PI SAKAMOTO, PI YUICHIRO KISHI PC C07K44/47, C12N15/12, C12P21/02, A01K67/027, C07K16/18, G01N33/53 CC Novel collectn FH key FT source FT location/Qualifiers 1. .663 /organism="Homo sapiens (human)". /mol_type="genomic DNA" /db_xref="taxon:9606"		
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ORIGIN			
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Query Match:	75.28%	Indels:	0
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## ORIGIN

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Best Local Similarity:	100.00%	Mismatches:	0
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US-09-806-277A-6 (1-271) x BC009951 (1-1417)

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Db 487 ATTGGCTCTAAAGGTGAAGAAAGAGATTCCGGTACATAGAACCCCTGGTCTTAATGA 546
QY 108 G1UProG1YLeuProCYsG1YCySerG1YLeuArgLYsAl1eG1YGLuMetAspAsn 127
Db 547 GAACCAAGCCTCCCATGTGATGACGCCAGCTGCCAAGGCCATCGGGAGATGACAC 606
QY 128 G1NValSerG1NLeuThrSerG1NLeuLYsPhe11eLYsAenAlaVal1eG1YValArg 147
Db 607 CAGGTCTCTCAGTCGACGACGAGCTCAAGTTCAATCAAGAAATGCTGCGCGGTGCGC 666
QY 148 G1UThrG1USeLYs11eLYsLeuValLYsG1UlySArgTYrAl1AspAlaG1N 167
Db 667 GAGACGAGAGCAAGATCTACCTCTGTGAAGAGAGAGCGCTACGCGGAGCCGAC 726
QY 168 LeuSerCYsG1NLYsArgG1YThrLeuSerMetProLYsAspG1UAl1a1AsnG1Y 187
Db 727 CTGTCTCTGCCAGGGCCCGGGGGGCAAGCTGACATGCCCAAGAGCGAGCTGCCAATGCC 786
QY 188 LeuMetAla1aLYsLeuAlaG1NLYsLeuAlaArgValPhe11eG1Y1eAsnAsp 207
Db 787 CTGATGGCCCGCATCTGCGCAAGCGGCTGGCCGCTTCATCGGCATCAACGAC 846
QY 208 LeuG1UlySArg1YAl1aPheValTYrSerAspH1SerProMetArgThrPheAsnLYs 227
Db 847 CTGGAGAGAGAGGGCGGCTTGTGTACTGTACCACTCCCATGCGGACCTTCAACAG 906
QY 228 TYrArgSerG1YUProAsnAsnAlaTYrAspG1UlyAspCYsValG1UmetValAla 247
Db 907 TGGGCGAGCGGTGAGCCCAATGCTTACGACGAGGAGGACTCGTGAGATGTGGCC 966
QY 248 SerG1YLYrTPanAspValAlaCYsH1sThrThreTYrPheMetCYsG1UlyPheAsp 267
Db 967 TCGGCGCGCTGGAAGAGAGTGGCTGCGCACACCAATGTACTTCATGTGTGAGTTTGAC 1026
QY 268 LYsG1UlyAsnMet 271
Db 1027 AAGGAGACATG 1038

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Search completed: December 17, 2004, 13:15:16  
 Job time : 5454 secs





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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      181 GTCCCTGGCTCTCAAAAGGGGATGCGGAGAGAAAGGAGCAAAAGCGCCCGGAGCGCT 240
QY      264 GGAAGAGTGGGCGCCCGAGGAGAAAGAGCATGGGGGCAAAAGGAGCAGAAAGGCGAGT 323
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QY      324 GTGGGTCTCATGAAAAATTGGTCCATTGGCTTTAAAGTGAAGAAAGAGATTCCGGT 383
DB      301 GTGGGTCTCATGAAAAATTGGTCCATTGGCTTTAAAGTGAAGAAAGAGATTCCGGT 360
QY      384 GACATGAGACCCCTGTGTTCTTAATGAGAACCGGCTTCCATGTGATGACGCGAGCTG 443
DB      361 GACATGAGACCCCTGTGTTCTTAATGAGAACCGGCTTCCATGTGATGACGCGAGCTG 420
QY      444 CGCAAGGCGCATCGGGGAGATGAGCAACAGGTCTTCAAGCTGACCAAGGAGCTCAAGTTC 503
DB      421 CGCAAGGCGCATCGGGGAGATGAGCAACAGGTCTTCAAGCTGACCAAGGAGCTCAAGTTC 480
QY      504 ATCAAGATGTGTGCGCGGTGTGCGCGAGACGAGACCAAGATTACTCTGTGTGAAG 563
DB      481 ATCAAGATGTGTGCGCGGTGTGCGCGAGACGAGACCAAGATTACTCTGTGTGAAG 540
QY      564 GAGGAGAAAGCGCTACGCGGAGCGCCAGCTGTCTGCAAGGCGCGGGGAGCAGCTGAGC 623
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QY      624 ATGCGCAAGGAGACGAGGCTGCGCAATGCGATGAGCGCGCATACCTGCGCCCAAGCGGCTG 683
DB      601 ATGCGCAAGGAGACGAGGCTGCGCAATGCGATGAGCGCGCATACCTGCGCCCAAGCGGCTG 660
QY      684 GCCCGTGTCTTCATGCGGATCAACGACCTTGAGAGAGAGGCGGCTTGTGTACTCTGAC 743
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DB      1201 TAGTGCAGTAGTTAAGTCAAAAAAAA 1230

RESULT 2
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; Sequence 356, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
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Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
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Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botsstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C56  
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CURRENT FILING DATE: 2001-11-19  
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15 PRIOR FILING DATE: 1998-07-02  
16 PRIOR APPLICATION NUMBER: 60/091978  
17 PRIOR FILING DATE: 1998-07-07  
18 PRIOR APPLICATION NUMBER: 60/091982  
19 PRIOR FILING DATE: 1998-07-07  
20 PRIOR APPLICATION NUMBER: 60/092182  
21 PRIOR FILING DATE: 1998-07-09

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Query Match      98.2%; Score 1230; DB 9; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	CTCAGGATGAGGGGGAAATCTGGCCCTGTGTGTGGCGTTCTAATCAGCTGGCCTTCTGTCA	120
Qy	144	CTGCTGCCATCTGGACATCTCTCAGCCGGCTGGCGATGAGCGCTGTCTGTGGCATCTTC	203
Db	121	CTGCTGCCATCTGGACATCTCTCAGCCGGCTGGCGATGAGCGCTGTGTGGCATCTTC	180
Qy	204	GTCCCTGGCTTCAAAAGGGGATGCGGAGAGAAAGGAGACAAAGGCCCCCGAGCGGCT	263
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Qy	264	GGAAAGTGTGGGCCCAACGGGAGAAAAGAGACATGGGGGACAAAGACAGAAAGGCAT	323
Db	241	GGAAAGTGTGGGCCCAACGGGAGAAAAGAGACATGGGGGACAAAGAGCAAAAGGCAGT	300
Qy	324	GTGGGTGCTCATGGAATAATTTGTCCTCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGT	383
Db	301	GTGGGTGCTCATGGAATAATTTGTCCTCATTTGGCTCTAAAGGTGAGAAAGAGATTCCGGT	360
Qy	384	GACATAGGACCCCCCTGTGTCTTAATGGAGAACAGGCTCTCCATGTGATGTCAGCCAGCTG	443
Db	361	GACATAGGACCCCCCTGTGTCTTAATGGAGAACAGGCTCTCCATGTGATGTCAGCCAGCTG	420
Qy	444	CGCAAGGCCATGCGGGGAGATGAGCAACAGAGTCTCTCACTGACAGCGGAGCTCAAGTTC	503
Db	421	CGCAAGGCCATGCGGGGAGATGAGCAACAGAGTCTCTCACTGACAGCGGAGCTCAAGTTC	480
Qy	504	ATCAAGAAATGCTGTGCGCGGGTGTGCGGAGACGGAGAGCAAGATCTTACTGTGTGAAG	563
Db	481	ATCAAGAAATGCTGTGCGCGGGTGTGCGGAGACGGAGAGCAAGATCTTACTGTGTGAAG	540
Qy	564	GAGGAGAAAGCGTTAGCGCGGACGCCCAAGCTGTCTGTGCAAGGCGCGGGGGCAGCTGAGC	623
Db	541	GAGGAGAAAGCGTTAGCGCGGACGCCCAAGCTGTCTGTGCAAGGCGCGGGGGCAGCTGAGC	600
Qy	624	ATGCCCAAGACGAGGCTTGCCCAATGGCTGTATGGCCGATACCTGTGCGCAAGCGGCTTG	683
Db	601	ATGCCCAAGACGAGGCTTGCCCAATGGCTGTATGGCCGATACCTGTGCGCAAGCGGCTTG	660
Qy	684	GCCCTGTCTTCAATGGGCATCAACGACTGTGAGAGAGAGAGGCGCCTTTCGTGTACTTGAC	743
Db	661	GCCCTGTCTTCAATGGGCATCAACGACTGTGAGAGAGAGAGGCGCCTTTCGTGTACTTGAC	720

QY	744	CACCTCCCGGACGGACCTTGAACAAGTGGGCGACGGGTGAGGCCCAACATGGCTTAGAC	803
Db	721	CACCTCCCGGACGGACCTTGAACAAGTGGGCGACGGGTGAGGCCCAACATGGCTTAGAC	780
QY	804	GAGGAGAGCTCGTGGAGATGGTGGCCCTCGGGCGGTGGAA CGA CGTGGCTGCACACC	863
Db	781	GAGGAGAGCTCGTGGAGATGGTGGCCCTCGGGCGGTGGAA CGA CGTGGCTGCACACC	840
QY	864	ACCATGTACTTCATGTGTGAAGTTTGACAAGAGAA CATGTAGCCTCAGGCTGGGGCTGC	923
Db	841	ACCATGTACTTCATGTGTGAAGTTTGACAAGAGAA CATGTAGCCTCAGGCTGGGGCTGC	900
QY	924	CCATTGGGGGGCCCCCA CATGTCCCTGCGACGGTTGGCGAGGAGACAGAGCCCAAGCATGTGGC	983
Db	901	CCATTGGGGGGGGCCCCCA CATGTCCCTGCGACGGTTGGCGAGGAGACAGAGCCCAAGCATGTGGC	960
QY	984	CAGCCAGGAGACGTGGCCCTGTGTGAAGGGTGGAGGCTACTGAGTAGAGGGCTGTGTCT	1043
Db	961	CAGCCAGGAGACGTGGCCCTGTGTGAAGGGTGGAGGCTACTGAGTAGAGGGCTGTGTCT	1020
QY	1044	AAACTGAGAAAATGGCTCATGTCTTAAAGAGAAAATGAAAGTTCCTGGGGTGCTGTTC	1103
Db	1021	AAACTGAGAAAATGGCTCATGTCTTAAAGAGAAAATGAAAGTTCCTGGGGTGCTGTTC	1080
QY	1104	TGAAGAGACAGATTTCAATPACCTGTATTGTAGCCCCAATGTCAATTATGTAATTATAC	1163
Db	1081	TGAAGAGACAGATTTCAATPACCTGTATTGTAGCCCCAATGTCAATTATGTAATTATAC	1140
QY	1164	CAGAAATTGCTCTTCATATAAGCTTGGCTTTGTCCAAAGCTATATACATAAAATCTTTAAG	1223
Db	1141	CAGAAATTGCTCTTCATATAAGCTTGGCTTTGTCCAAAGCTATATACATAAAATCTTTAAG	1200
QY	1224	TAGTGCAGTAGTTAAGTCCAAAAAATAAAAAA 1253	
Db	1201	TAGTGCAGTAGTTAAGTCCAAAAAATAAAAAA 1230	

RESULT 4  
 US-09-989-727-356  
 / Sequence 356, Application US/09989727  
 / Patent No. US20020072497A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Ashkenazi, Avi J.  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Deans, Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerritsen, Mary B.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Kijavich, Ivar J.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Colin K.  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / TITLE OF INVENTION: Acids Encoding the Same  
 / FILE REFERENCE: P2730PICS  
 / CURRENT APPLICATION NUMBER: US/09/989,727  
 / CURRENT FILING DATE: 2001-11-19  
 / PRIOR APPLICATION NUMBER: 60/049787

[illegible]



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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      98.2%; Score 1230; DB 9; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      24 GCGACGGGACAGACGCCCCGCTTCCCTTACGCGGCTCTCAGAGTTGTGTCTCTGCTCGC 83
Db      1 GCGACGGGACAGACGCCCCGCTTCCCTTACGCGGCTCTCAGAGTTGTGTCTCTGCTCGC 60

Oy      84 CTCAGAGAGAGGGGAAATCTGGCCCTGGGGGCGTTCTTAATAGGCTGGCCCTTCTCTGCA 143
Db      61 CTCAGAGAGAGGGGAAATCTGGCCCTGGGGGCGTTCTTAATAGGCTGGCCCTTCTCTGCA 120

Oy      144 CTGCTGCATCTGACATCTCTCAGCGGCTGGCGATGACGCTCTCTGTGCAATCTCTC 203
Db      121 CTGCTGCATCTGACATCTCTCAGCGGCTGGCGATGACGCTCTCTGTGCAATCTCTC 180

Oy      204 GTCCCTGGCTCAAAAGGGATCGGGAGAGAAAGGAGACAAAGCGCCCCGGACGGCCT 263
Db      181 GTCCCTGGCTCAAAAGGGATCGGGAGAGAAAGGAGACAAAGCGCCCCGGACGGCCT 240

Oy      264 GGAAGAGTCGGGCCCAACGGGAGAAAGAGACATGGGGGCAAAAGACAGAAAGGACGT 323
Db      241 GGAAGAGTCGGGCCCAACGGGAGAAAGAGACATGGGGGCAAAAGACAGAAAGGACGT 300

Oy      324 GTGGGTGCTCATGAAAAATTTGATCCCATTTGCTCTAAAGTGAGAAAGGATTCGGGT 383
Db      301 GTGGGTGCTCATGAAAAATTTGATCCCATTTGCTCTAAAGTGAGAAAGGATTCGGGT 360

Oy      384 GACATAGACCCCTGTGCTCTAATGAGAACAGAGCTTCCATGTGATGACAGCAGCTG 443
Db      361 GACATAGACCCCTGTGCTCTAATGAGAACAGAGCTTCCATGTGATGACAGCAGCTG 420

Oy      444 CGCAAGGCTATGGGGAGATGACACACAGGTCTCTCAGCTACCAAGGAGCTCAAGTTC 503
Db      421 CGCAAGGCTATGGGGAGATGACACACAGGTCTCTCAGCTACCAAGGAGCTCAAGTTC 480

Oy      504 ATCAAGATGTGTGCGCGGTGTGGCGGAGACGAGAGAGCAATCTACTCTGTGTGAAG 563
Db      481 ATCAAGATGTGTGCGCGGTGTGGCGGAGACGAGAGAGCAATCTACTCTGTGTGAAG 540

Oy      564 GAGGAGAAAGCGTACGCGGACGCCACGCTGTCTTGCAGAGGCGCGGGGGACGCTGAGC 623
Db      541 GAGGAGAAAGCGTACGCGGACGCCACGCTGTCTTGCAGAGGCGCGGGGGACGCTGAGC 600

Oy      624 ATGCCCAAGAGAGAGCTTCCCATATGGCTTGATGGCCGCGCATACTGGCCGAAACCGGCTG 683
Db      601 ATGCCCAAGAGAGAGCTTCCCATATGGCTTGATGGCCGCGCATACTGGCCGAAACCGGCTG 660

Oy      684 GCCCGTGTCTTATCGGAGATCAACGACCTGAGAAAGAGGCGCTCTGTACTCTGAC 743
Db      661 GCCCGTGTCTTATCGGAGATCAACGACCTGAGAAAGAGGCGCTCTGTACTCTGAC 720
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Oy      744 CACTCCCCCATGGGACCTTCAACAGAGGCGGAGGAGCCCAACAATGCTTACGAC 803
Db      721 CACTCCCCCATGGGACCTTCAACAGAGGCGGAGGAGCCCAACAATGCTTACGAC 780

Oy      804 GAGGAGAGCTGCGTGAATGTTGCTCGGCGGCTGGAACGAGCTGGCTGCGACACC 863
Db      781 GAGGAGAGCTGCGTGAATGTTGCTCGGCGGCTGGAACGAGCTGGCTGCGACACC 840

Oy      864 ACCATGTACTTCAATGTGATGTTGACAGAGAACTGTGAGCTTCAAGGCTGGGCTGC 923
Db      841 ACCATGTACTTCAATGTGATGTTGACAGAGAACTGTGAGCTTCAAGGCTGGGCTGC 900

Oy      924 CCATTTGGGGGCGCCCAACATGTCCTCGACGGGTTGGCAAGGACAGGCCAATGAGTGC 983
Db      901 CCATTTGGGGGCGCCCAACATGTCCTCGACGGGTTGGCAAGGACAGGCCAATGAGTGC 960

Oy      984 CAGCGAGGAGCTGCTCCCTCTGTGAAAGGTTGAGAGCTCACTGATGAGAGGCTGTGCT 1043
Db      961 CAGCGAGGAGCTGCTCCCTCTGTGAAAGGTTGAGAGCTCACTGATGAGAGGCTGTGCT 1020

Oy      1044 AACTGAGAAAATGCGCTATGCTTAAGAGAAATGAAAGTTCCTGGGCTGTGCTC 1103
Db      1021 AACTGAGAAAATGCGCTATGCTTAAGAGAAATGAAAGTTCCTGGGCTGTGCTC 1080

Oy      1104 TGAAGAGCAGAGTTCACTTACCTGTAATGTAAGCCCAATGTCAATTAATTAATAC 1163
Db      1081 TGAAGAGCAGAGTTCACTTACCTGTAATGTAAGCCCAATGTCAATTAATTAATAC 1140

Oy      1164 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCAAGCTATACAATTAATCTTTAAG 1223
Db      1141 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTCAAGCTATACAATTAATCTTTAAG 1200

Oy      1224 TAGTGCACTTAAGTCAAAAAA 1253
Db      1201 TAGTGCACTTAAGTCAAAAAA 1230

RESULT 5
US-09-989-731-356
; Sequence 356, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerilsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731-
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGGAGAGCCCGCTTCCGCTAGCGCGCTCTCAGAGTTGGTCTCTGCTCGG 83  
DB 1 GCGAGGCGGAGAGCCCGCTTCCGCTAGCGCGCTCTCAGAGTTGGTCTCTGCTCGG 60  
QY 84 CTCAGAGTGGGAGGAAATGCGCCCTGGTGGGCTTCTAATCAGCTGGCTTCTCTGCA 143  
DB 61 CTCAGAGTGGGAGGAAATGCGCCCTGGTGGGCTTCTAATCAGCTGGCTTCTCTGCA 120  
QY 144 CTGCTGCAATCTGACATCTTACCGCGCTGGCGATGAGCGCTCTCTGTGCAATCTTC 203  
DB 121 CTGCTGCAATCTGACATCTTACCGCGCTGGCGATGAGCGCTCTCTGTGCAATCTTC 180  
QY 204 GTCCCTGGCTCTAAGGGGATCGGGAGAGAGGAGAGGAGGAGGAGGAGGAGGAGG 263  
DB 181 GTCCCTGGCTCTAAGGGGATCGGGAGAGAGGAGAGGAGGAGGAGGAGGAGGAGG 240  
QY 264 GGAAGAGTCGCGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTCGCGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGGTGCTGATGAG 383  
DB 301 GTGGGTGCTGATGAG 360  
QY 384 GACATAG 443  
DB 361 GACATAG 420  
QY 444 GCGAGGCGGAG 503  
DB 421 GCGAGGCGGAG 480  
QY 504 ATCAAGATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGATGCTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAGGAG 623  
DB 541 GAGGAG 600  
QY 624 ATGCCAG 683  
DB 601 ATGCCAG 660  
QY 684 GCCCGTGTCTTATCGGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGTGTCTTATCGGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCATGCGGAGCTTCAACAAGTGGGAGCGGAGAGAGAGAGAGAGAGAGAG 803  
DB 721 CACTCCCCCATGCGGAGCTTCAACAAGTGGGAGCGGAGAGAGAGAGAGAGAGAGAG 780  
QY 804 GAGGAG 863  
DB 781 GAGGAG 840  
QY 864 ACCATGATCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
DB 841 ACCATGATCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 924 CCATTTGG 983  
DB 901 CCATTTGG 960  
QY 984 CAGCCAGGAG 1043  
DB 961 CAGCCAGGAG 1020  
QY 1044 AAAGTGAAG 1103  
DB 1021 AAAGTGAAG 1080  
QY 1104 TGAAG 1163  
DB 1081 TGAAG 1140  
QY 1164 CAGAGTGTCTCTTCAATAG 1223  
DB 1141 CAGAGTGTCTCTTCAATAG 1200  
QY 1224 TAGTGCAGTGAATGAG 1253  
DB 1201 TAGTGCAGTGAATGAG 1230

RESULT 6  
US-09-989-732-356  
Sequence 356, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivay J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2% Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGGAGAGCCCGCTTCCGCTGACGCGTCTCAGAGTGGTGTCTCTGCTCGC 83  
DB 1 GCGAGGCGGAGAGCCCGCTTCCGCTGACGCGTCTCAGAGTGGTGTCTCTGCTCGC 60  
QY 84 CTGAGATGAGGGGAGATCTGGCCCTGGTGGGCTTTCTAATAGCCTGGCCCTTCTGCA 143  
DB 61 CTCAGATGAGGGGAGATCTGGCCCTGGTGGGCTTTCTAATAGCCTGGCCCTTCTGCA 120  
QY 144 CTGCTGCAATCTGACATCTCTCAGCGGCTGGCGATGACGCTCTCTGTGCAATCTCTC 203  
DB 121 CTGCTGCAATCTGACATCTCTCAGCGGCTGGCGATGACGCTCTCTGTGCAATCTCTC 180  
QY 204 GTCCCTGGCTTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGGCGCCCGGAGCGCT 263  
DB 181 GTCCCTGGCTTCAAAAGGGGATCGGGAGAGAAAGGAGACAAAGGCGCCCGGAGCGCT 240  
QY 264 GGAAGAGTCGGCCCAAGGGAGAGAAAGGAGCATGGGGGCAAAAGGAGAGAGAGAGT 323  
DB 241 GGAAGAGTCGGCCCAAGGGAGAGAAAGGAGCATGGGGGCAAAAGGAGAGAGAGT 300  
QY 324 GTGGTCTGATGAGAAATTTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGT 383  
DB 301 GTGGTCTGATGAGAAATTTGGTCCATTGGCTCTAAAGGTGAGAAAGAGATTCGGT 360  
QY 384 GACATAGACCCCTGGTCTTATGAGAGAACAGGCTTCCATGTGAGTGCAGCAAGCTG 443  
DB 361 GACATAGACCCCTGGTCTTATGAGAGAACAGGCTTCCATGTGAGTGCAGCAAGCTG 420  
QY 444 CGCAAGGCGATCGGGAGATGAGCAACAGGCTCTCAGCTGACCAAGGAGCTCAAGTTC 503  
DB 421 CGCAAGGCGATCGGGAGATGAGCAACAGGCTCTCAGCTGACCAAGGAGCTCAAGTTC 480  
QY 504 ATCAAGAAATGCTGTGCGCGTGTGGCGAGACGAGAGAGATCTAAGTGTGTGAAG 563  
DB 481 ATCAAGAAATGCTGTGCGCGTGTGGCGAGACGAGAGAGATCTAAGTGTGTGAAG 540  
QY 564 GAGGAGAAAGCGCTACGCGGAGCCCGAGCTGTCTTCCAGGCGCGGGGGGACGCTGAGC 623  
DB 541 GAGGAGAAAGCGCTACGCGGAGCCCGAGCTGTCTTCCAGGCGCGGGGGGACGCTGAGC 600  
QY 624 ATGCCCAAGGAGAGAGGCTGCAATGAGCTGATGAGCGGAGTACCTGGGCGCAAGCGGCTG 683  
DB 601 ATGCCCAAGGAGAGAGGCTGCAATGAGCTGATGAGCGGAGTACCTGGGCGCAAGCGGCTG 660  
QY 684 GCCCGTGTCTTATCGGATCAACAGACTGAGAGAGAGGCGCTTCTGTACTCTGAC 743  
DB 661 GCCCGTGTCTTATCGGATCAACAGACTGAGAGAGAGGCGCTTCTGTACTCTGAC 720

QY 744 CACTCCCCATGCGGAGACCTTCAACAGTGGGCGAGCGGTGAGCCCAACATGCTTACGAC 803  
DB 721 CACTCCCCATGCGGAGACCTTCAACAGTGGGCGAGCGGTGAGCCCAACATGCTTACGAC 780  
QY 804 GAGAGAGACTGCTGAGAGATGAGTGGCTCGGCGGCTGGAACGACGCTGCTGCACACC 863  
DB 781 GAGAGAGACTGCTGAGAGATGAGTGGCTCGGCGGCTGGAACGACGCTGCTGCACACC 840  
QY 864 ACCATGTACTTCAATGTGTGAGATTGACAGAGAAATGATGAGCTCAGGCTGGGGCTGC 923  
DB 841 ACCATGTACTTCAATGTGTGAGATTGACAGAGAAATGATGAGCTCAGGCTGGGGCTGC 900  
QY 924 CCATTGGGGGGCCCAACATGCTCGAGGGGTGGAGGAGGAGAGGAGGAGGAGGAGGAGG 983  
DB 901 CCATTGGGGGGCCCAACATGCTCGAGGGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
QY 984 CAGCAGGAGACTGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1043  
DB 961 CAGCAGGAGACTGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020  
QY 1044 AAAGTGAAGAAATGAGCTTATGCTTATGAGAGAAATGAAAGTGTCTCTGGGCTGTCTC 1103  
DB 1021 AAAGTGAAGAAATGAGCTTATGCTTATGAGAGAAATGAAAGTGTCTCTGGGCTGTCTC 1080  
QY 1104 TGAAGAGCAGAGTTCATTAAGCTGATTTGAGGCCCAAGTGCATTATGATTAATTAAC 1163  
DB 1081 TGAAGAGCAGAGTTCATTAAGCTGATTTGAGGCCCAAGTGCATTATGATTAATTAAC 1140  
QY 1164 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTGCAAGCTATACATTAATCTTTAAG 1223  
DB 1141 CAGAAATGCTCTTCCATTAAGCTTGTGCTTGTGCAAGCTATACATTAATCTTTAAG 1200  
QY 1224 TAGTCACTAGTTAAGTCAAAAAA 1253  
DB 1201 TAGTCACTAGTTAAGTCAAAAAA 1230

RESULT 7  
US-09-991-073-356  
Sequence 356, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austen L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

1	PRIOR APPLICATION NUMBER: 60/089440-16
2	PRIOR FILING DATE: 1998-06-16
3	PRIOR APPLICATION NUMBER: 60/089512-12
4	PRIOR FILING DATE: 1998-06-16
5	PRIOR APPLICATION NUMBER: 60/089511-16
6	PRIOR FILING DATE: 1998-06-16
7	PRIOR APPLICATION NUMBER: 60/089533-33
8	PRIOR FILING DATE: 1998-06-17
9	PRIOR APPLICATION NUMBER: 60/089538-17
10	PRIOR FILING DATE: 1998-06-17
11	PRIOR APPLICATION NUMBER: 60/089539-18
12	PRIOR FILING DATE: 1998-06-17
13	PRIOR APPLICATION NUMBER: 60/089801-01
14	PRIOR FILING DATE: 1998-06-18
15	PRIOR APPLICATION NUMBER: 60/089907-07
16	PRIOR FILING DATE: 1998-06-18
17	PRIOR APPLICATION NUMBER: 60/089908-18
18	PRIOR FILING DATE: 1998-06-18
19	PRIOR APPLICATION NUMBER: 60/089947-47
20	PRIOR FILING DATE: 1998-06-19
21	PRIOR APPLICATION NUMBER: 60/089948-18
22	PRIOR FILING DATE: 1998-06-19
23	PRIOR APPLICATION NUMBER: 60/089952-24
24	PRIOR FILING DATE: 1998-06-19
25	PRIOR APPLICATION NUMBER: 60/090246-16
26	PRIOR FILING DATE: 1998-06-20
27	PRIOR APPLICATION NUMBER: 60/090252-52
28	PRIOR FILING DATE: 1998-06-22
29	PRIOR APPLICATION NUMBER: 60/090254-24
30	PRIOR FILING DATE: 1998-06-22
31	PRIOR APPLICATION NUMBER: 60/090349-49
32	PRIOR FILING DATE: 1998-06-23
33	PRIOR APPLICATION NUMBER: 60/090355-55
34	PRIOR FILING DATE: 1998-06-23
35	PRIOR APPLICATION NUMBER: 60/090429-29
36	PRIOR FILING DATE: 1998-06-24
37	PRIOR APPLICATION NUMBER: 60/090431-31
38	PRIOR FILING DATE: 1998-06-24
39	PRIOR APPLICATION NUMBER: 60/090435-35
40	PRIOR FILING DATE: 1998-06-24
41	PRIOR APPLICATION NUMBER: 60/090444-44
42	PRIOR FILING DATE: 1998-06-24
43	PRIOR APPLICATION NUMBER: 60/090445-45
44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/090472-72
46	PRIOR FILING DATE: 1998-06-24
47	PRIOR APPLICATION NUMBER: 60/090535-35
48	PRIOR FILING DATE: 1998-06-24
49	PRIOR APPLICATION NUMBER: 60/090540-40
50	PRIOR FILING DATE: 1998-06-24
51	PRIOR APPLICATION NUMBER: 60/090557-57
52	PRIOR FILING DATE: 1998-06-24
53	PRIOR APPLICATION NUMBER: 60/090676-76
54	PRIOR FILING DATE: 1998-06-25
55	PRIOR APPLICATION NUMBER: 60/090678-78
56	PRIOR FILING DATE: 1998-06-25
57	PRIOR APPLICATION NUMBER: 60/090690-90
58	PRIOR FILING DATE: 1998-06-25
59	PRIOR APPLICATION NUMBER: 60/090694-94
60	PRIOR FILING DATE: 1998-06-25
61	PRIOR APPLICATION NUMBER: 60/090695-95
62	PRIOR FILING DATE: 1998-06-25
63	PRIOR APPLICATION NUMBER: 60/090696-96
64	PRIOR FILING DATE: 1998-06-25
65	PRIOR APPLICATION NUMBER: 60/090862-62

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGGAGAGCGCCCGCTTGGCTGAGCGGCTGCTCAGAGTTGGTCTCTGCTGCG 83  
DB 1 GCGAGGCGGAGAGCGCCCGCTTGGCTGAGCGGCTGCTCAGAGTTGGTCTCTGCTGCG 60  
QY 84 CTGAGATGAGGAGGAGATCTGCGCTGAGGCGCTTCTAATAGGCTGCGCTTCTGCTCA 143  
DB 61 CTGAGATGAGGAGGAGATCTGCGCTGAGGCGCTTCTAATAGGCTGCGCTTCTGCTCA 120  
QY 144 CTGCTGCAATCTGAGCATCTCAGCGGCTGCGAGTGAAGCGCTGCTGCTGCAATCTC 203  
DB 121 CTGCTGCAATCTGAGCATCTCAGCGGCTGCGAGTGAAGCGCTGCTGCTGCAATCTC 180  
QY 204 GTCCCTGCGCTCAAGGAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGCGCTCAAGGAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTGGGCGCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTGGGCGCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGGTGCTGATGAG 383  
DB 301 GTGGGTGCTGATGAG 360  
QY 384 GACATAG 443  
DB 361 GACATAG 420  
QY 444 GCGAGAGGCGAGGAG 503  
DB 421 GCGAGAGGCGAGGAG 480  
QY 504 ATCAAGAGTGTGTGCGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
DB 481 ATCAAGAGTGTGTGCGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 564 GAG 623  
DB 541 GAG 600  
QY 624 ATGCGCAAG 683  
DB 601 ATGCGCAAG 660  
QY 684 GCGCGGTGCTGATGAG 743  
DB 661 GCGCGGTGCTGATGAG 720

QY 744 CACTCCCCATGCGGAGAGCTTCAACAGTGGGAGAGGAGAGAGAGAGAGAGAGAGAGAG 803  
DB 721 CACTCCCCATGCGGAGAGCTTCAACAGTGGGAGAGGAGAGAGAGAGAGAGAGAGAGAG 780  
QY 804 GAG 863  
DB 781 GAG 840  
QY 864 ACCATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 923  
DB 841 ACCATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 924 CCATTGG 983  
DB 901 CCATTGG 960  
QY 984 CAGCGAG 1043  
DB 961 CAGCGAG 1020  
QY 1044 AAAGTGAAG 1103  
DB 1021 AAAGTGAAG 1080  
QY 1104 TGAAG 1163  
DB 1081 TGAAG 1140  
QY 1164 CAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1223  
DB 1141 CAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
QY 1224 TAGTGAG 1283  
DB 1201 TAGTGAG 1260

RESULT 8  
US-09-990-442-356  
Sequence 356, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlt, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acid Encoding the Same  
FILE REFERENCE: P2730PIC8  
CURRENT APPLICATION NUMBER: US/09/990,442  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]





[illegible]

;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
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;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGGGAGAGACCCCGCTTCCGCTAGCCGCTCTCAGAGTGTGTCTCTGCTCGG 83  
DB 1 GCGAGGGGAGAGACCCCGCTTCCGCTAGCCGCTCTCAGAGTGTGTCTCTGCTCGG 60  
QY 84 CTCAGATGAGGGGAGATCTGCGCTGTGGGCGTTCTATCAGCCTGAGCTTCTCTGCA 143  
DB 61 CTCAGATGAGGGGAGATCTGCGCTGTGGGCGTTCTATCAGCCTGAGCTTCTCTGCA 120  
QY 144 CTGCTGCATCTGACATCTCTCAGCCGCTGCGATGAGCGCTGCTCTGTGCAATCTCT 203  
DB 121 CTGCTGCATCTGACATCTCTCAGCCGCTGCGATGAGCGCTGCTCTGTGCAATCTCT 180  
QY 204 GTCCCTGCTCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 181 GTCCCTGCTCTCAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 264 GGAAGAGTCGCGCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 241 GGAAGAGTCGCGCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 324 GTGGTCTCTCAAGAAAAATTGCTCCATTGCTCTAAGGTGAGAGAGAGAGATTC 383  
DB 301 GTGGTCTCTCAAGAAAAATTGCTCCATTGCTCTAAGGTGAGAGAGAGATTC 360  
QY 384 GACATAGAGACCCCTGCTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443  
DB 361 GACATAGAGACCCCTGCTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 444 CGCAAGGCGCATCGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 503  
DB 421 CGCAAGGCGCATCGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGAGATCTAGCTGTGA 563  
DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGAGATCTAGCTGTGA 540  
QY 564 GAGGAGAGAGCGCTTACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623  
DB 541 GAGGAGAGAGCGCTTACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
QY 624 ATGCGCAAG 683  
DB 601 ATGCGCAAG 660  
QY 684 GCCCGTGTCTTCTATGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743  
DB 661 GCCCGTGTCTTCTATGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 744 CACTCCCCCATGCGGACCTTGAACAAGTGGGCGAGCGGTGAGGCCCAACAATGCTAGAC 803  
DB 721 CACTCCCCCATGCGGACCTTGAACAAGTGGGCGAGCGGTGAGGCCCAACAATGCTAGAC 780  
QY 804 GAGAGAGAGCTGCTGAGAGATGCTGCGGCGGCTGGAAGAGAGAGAGAGAGAGAG 863  
DB 781 GAGAGAGAGCTGCTGAGAGATGCTGCGGCGGCTGGAAGAGAGAGAGAGAGAGAG 840  
QY 864 ACCATGTAATTCATGTGTGAGTTTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
DB 841 ACCATGTAATTCATGTGTGAGTTTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 924 CCATTGGGGGGCCCAAGATGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
DB 901 CCATTGGGGGGCCCAAGATGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 984 CAGCAGAGAGAGCTGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043  
DB 961 CAGCAGAGAGAGCTGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1044 AAAGTGAAGAAATGCGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103  
DB 1021 AAAGTGAAGAAATGCGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
QY 1104 TGAAGAGAGAGAGTTTCAATACCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1163  
DB 1081 TGAAGAGAGAGAGTTTCAATACCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
QY 1164 CAGAAATGCTCTTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223  
DB 1141 CAGAAATGCTCTTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
QY 1224 TAGTGCAAGTAAATGTCAAAAA 1253  
DB 1201 TAGTGCAAGTAAATGTCAAAAA 1230

RESULT 10  
US-09-993-604-356  
Sequence 356, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGGCGAGGACCCCGCTTCGCTAGCGGCTGCTCAGAGTGTGTCTCTGCTCG 83  
DB 1 GCGAGGCGAGGACCCCGCTTCGCTAGCGGCTGCTCAGAGTGTGTCTCTGCTCG 60  
QY 84 CTCAGAGTGAAGGAGATCTGAGCCTGTGAGGCGTTCTAATCAGCCTGCGCTTCTGCA 143  
DB 61 CTCAGAGTGAAGGAGATCTGAGCCTGTGAGGCGTTCTAATCAGCCTGCGCTTCTGCA 120  
QY 144 CTGCTGCATCTGACATCTCAGCGCTGCGAGTGAAGCGCTGCTGTGTGCAATCTTC 203  
DB 121 CTGCTGCATCTGACATCTCAGCGCTGCGAGTGAAGCGCTGCTGTGTGCAATCTTC 180  
QY 204 GTCCCTGCGCTTCAAGGGATTCGGGAGAGAAAGGAGACAAAGGCGCCCGGAGAGGCTT 263  
DB 181 GTCCCTGCGCTTCAAGGGATTCGGGAGAGAAAGGAGACAAAGGCGCCCGGAGAGGCTT 240  
QY 264 GGAAGAGTGGGCGCCGAGGAGAGAAAGGAGACATGGGGGACAAAGAGACAGAAAGGCACT 323  
DB 241 GGAAGAGTGGGCGCCGAGGAGAGAAAGGAGACATGGGGGACAAAGAGAGAGGCACT 300  
QY 324 GTGGGTGCTCATGAGAAAAATGGTCCCATTTGGCTTAAAGGTGAGAAAGAGATTCGAGT 383  
DB 301 GTGGGTGCTCATGAGAAAAATGGTCCCATTTGGCTTAAAGGTGAGAAAGAGATTCGAGT 360  
QY 384 GACATAGGAGCCCGCTGTGTCTTAATGAGAAACAGGCTTCCATGTGAGTGCAGCCAGCTG 443  
DB 361 GACATAGGAGCCCGCTGTGTCTTAATGAGAAACAGGCTTCCATGTGAGTGCAGCCAGCTG 420  
QY 444 GCGAAGGCGCATGGGAGAGATGAGAACAGGCTCTCTCAGCTGACAGAGAGTCAAGTTTC 503  
DB 421 GCGAAGGCGCATGGGAGAGATGAGAACAGGCTCTCTCAGCTGACAGAGAGTCAAGTTTC 480  
QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGAGATTAATCTGCTGTGAG 563  
DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGATTAATCTGCTGTGAG 540  
QY 564 GAGGAGAAAGCGCTTACCGGAGCGCCAGCTGTCTTGCAGAGCGCGGGGGGACGCTGAGC 623  
DB 541 GAGGAGAAAGCGCTTACCGGAGCGCCAGCTGTCTTGCAGAGCGCGGGGGGACGCTGAGC 600  
QY 624 ATGCCCAAGAGAGAGGCTGCGCAATGAGCGCTGATGGCGGATTAATCTGCGGAGCGGCTG 683  
DB 601 ATGCCCAAGAGAGAGGCTGCGCAATGAGCGCTGATGGCGGATTAATCTGCGGAGCGGCTG 660  
QY 684 GCCCGGTGTCTTATCGGATCAACGACCTGAGAGAGAGAGGCGCTTGTGTACTTGTAC 743  
DB 661 GCCCGGTGTCTTATCGGATCAACGACCTGAGAGAGAGAGGCGCTTGTGTACTTGTAC 720

QY 744 CACTCCCCCATGCGGAGCTTCAACAGTGGGAGCGGCTGAGGCCCAACATGCTTACGAC 803  
DB 721 CACTCCCCCATGCGGAGCTTCAACAGTGGGAGCGGCTGAGGCCCAACATGCTTACGAC 780  
QY 804 GAGGAGAGCTGCTGAGAGATGATGCTCGGCGGCTGAGAAAGAGTGGCTTGCACACC 863  
DB 781 GAGGAGAGCTGCTGAGAGATGATGCTCGGCGGCTGAGAAAGAGTGGCTTGCACACC 840  
QY 864 ACCATGTACTTCAATGTGTGAGTGTGACAGAGAAACATGTAGCTTCAAGCTGGGGCTGC 923  
DB 841 ACCATGTACTTCAATGTGTGAGTGTGACAGAGAAACATGTAGCTTCAAGCTGGGGCTGC 900  
QY 924 CCATTGGGGGGGCGGACATGCTCCCTGAGGAGGTTGGAGGAGAGAGGCCCAACATGCTGC 983  
DB 901 CCATTGGGGGGGCGGACATGCTCCCTGAGGAGGTTGGAGGAGAGAGGCCCAACATGCTGC 960  
QY 984 CAGCCAGGAGCTGTCCCTCTGTGAGAGGCTGAGAGCTCACTGAGTGAAGGCTGTGTCT 1043  
DB 961 CAGCCAGGAGCTGTCCCTCTGTGAGAGGCTGAGAGCTCACTGAGTGAAGGCTGTGTCT 1020  
QY 1044 AAAGTGAAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTGTCTTGGGGTGTCTTC 1103  
DB 1021 AAAGTGAAGAAATGAGCTTATGCTTAAAGAGAAATGAAAGTGTCTTGGGGTGTCTTC 1080  
QY 1104 TGAAGAGCAGAGTTTCAATACCTGATTTGTAAGCCCAATGCAATTAATTAATTAAC 1163  
DB 1081 TGAAGAGCAGAGTTTCAATACCTGATTTGTAAGCCCAATGCAATTAATTAATTAAC 1140  
QY 1164 CAGAAATGCTCTTCATTAAGCTTGTGCTTGTTCAGAGTATACATTAATTAATTAAG 1223  
DB 1141 CAGAAATGCTCTTCATTAAGCTTGTGCTTGTTCAGAGTATACATTAATTAATTAAG 1200  
QY 1224 TAGTGCAGTAAATTAAGTCAAAAAA 1253  
DB 1201 TAGTGCAGTAAATTAAGTCAAAAAA 1230

RESULT 11  
US-09-990-456-356  
; Sequence 356, Application US/09990456  
; Patent No. US20020137890A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bockstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Batton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geider, Hanspeter  
; APPLICANT: Gerlt, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zenlin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
CURRENT APPLICATION NUMBER: US/09/990.456  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787

1	PRIOR APPLICATION NUMBER: 60/0894440
2	PRIOR FILING DATE: 1998-06-15
3	PRIOR APPLICATION NUMBER: 60/089512
4	PRIOR FILING DATE: 1998-06-16
5	PRIOR APPLICATION NUMBER: 60/089514
6	PRIOR FILING DATE: 1998-06-16
7	PRIOR APPLICATION NUMBER: 60/089532
8	PRIOR FILING DATE: 1998-06-17
9	PRIOR APPLICATION NUMBER: 60/089538
10	PRIOR FILING DATE: 1998-06-17
11	PRIOR APPLICATION NUMBER: 60/089558
12	PRIOR FILING DATE: 1998-06-17
13	PRIOR APPLICATION NUMBER: 60/089599
14	PRIOR FILING DATE: 1998-06-17
15	PRIOR APPLICATION NUMBER: 60/089600
16	PRIOR FILING DATE: 1998-06-17
17	PRIOR APPLICATION NUMBER: 60/089653
18	PRIOR FILING DATE: 1998-06-17
19	PRIOR APPLICATION NUMBER: 60/089801
20	PRIOR FILING DATE: 1998-06-18
21	PRIOR APPLICATION NUMBER: 60/089907
22	PRIOR FILING DATE: 1998-06-18
23	PRIOR APPLICATION NUMBER: 60/089908
24	PRIOR FILING DATE: 1998-06-18
25	PRIOR APPLICATION NUMBER: 60/089947
26	PRIOR FILING DATE: 1998-06-19
27	PRIOR APPLICATION NUMBER: 60/089948
28	PRIOR FILING DATE: 1998-06-19
29	PRIOR APPLICATION NUMBER: 60/089952
30	PRIOR FILING DATE: 1998-06-19
31	PRIOR APPLICATION NUMBER: 60/090246
32	PRIOR FILING DATE: 1998-06-22
33	PRIOR APPLICATION NUMBER: 60/090252
34	PRIOR FILING DATE: 1998-06-22
35	PRIOR APPLICATION NUMBER: 60/090254
36	PRIOR FILING DATE: 1998-06-22
37	PRIOR APPLICATION NUMBER: 60/090349
38	PRIOR FILING DATE: 1998-06-23
39	PRIOR APPLICATION NUMBER: 60/090355
40	PRIOR FILING DATE: 1998-06-23
41	PRIOR APPLICATION NUMBER: 60/090429
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44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/090435
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47	PRIOR APPLICATION NUMBER: 60/090444
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62	PRIOR FILING DATE: 1998-06-25
63	PRIOR APPLICATION NUMBER: 60/090650
64	PRIOR FILING DATE: 1998-06-25
65	PRIOR APPLICATION NUMBER: 60/090659
66	PRIOR FILING DATE: 1998-06-25
67	PRIOR APPLICATION NUMBER: 60/090655
68	PRIOR FILING DATE: 1998-06-25
69	PRIOR APPLICATION NUMBER: 60/090666
70	PRIOR FILING DATE: 1998-06-25
71	PRIOR APPLICATION NUMBER: 60/090862
72	PRIOR FILING DATE: 1998-06-25

OY	24	ACGACGGGACGAGACCCCGCTTGGCTTACCGCGTGTCTAGAGAGTTGGTGTCTGCCTGG	83
Db	1	GCGACGGGACGAGACCCCGCTTGGCTTACCGCGTGTCTAGAGAGTTGGTGTCTGCCTGG	60
OY	84	CTCAGGATGAGGGGGAAATTGGGCCCTGTGGGCGTTCTAATCAGCCTGGCTTCTGTCA	143
Db	61	CTCAGGATGAGGGGGAAATTCTGGCCCTGTGGGCGTTCTAATCAGCCTGGCTTCTGTCA	120
OY	144	CTGCTGCCATCTGGGACATCCTCAGCGCGGCTGGGATGAGCGCCGCTCTGAGCAGATCTTC	203
Db	121	CTGCTGCCATCTGGACATCTCAGCGCGCTGGGATGAGCGCCGCTCTGTGACGATCTTC	180
OY	204	GTCCCTGGCTTCAAAAGGGATGCGGGAGAGAAAGGAGCAAAAGCGCCCCCGAGCGCTT	263
Db	181	GTCCCTGGCTTCAAAAGGGATGCGGGAGAGAAAGGAGCAAAAGCGCCCCCGAGCGCTT	240
OY	264	GGAAGATGCGGCGCCACCGGGAGAAAAGAGACATGGGGGACAAAGACAGAAAGGCAAT	323
Db	241	GGAAGATGCGGCGCCACCGGAGAAAAGAGACATGGGGGACAAAGACAGAAAGGCAAT	300
OY	324	GTGGTGTGTATGGAATAATTGGTCCCATTTGGCTTAAAGGTGAGAAAGGAGATTCCGCT	383
Db	301	GTGGTGTGTATGGAATAATTGGTCCCATTTGGCTTAAAGGTGAGAAAGGAGATTCCGCT	360
OY	384	GACATATGAGACCCCTGTGTCTTAATGGAGAACCAAGGCTCCCATGTGATGTCAAGCAGCTG	443
Db	361	GACATATGAGACCCCTGTGTCTTAATGGAGAACCAAGGCTCCCATGTGATGTCAAGCAGCTG	420
OY	444	CGCAAGGCCATCGGGAGATGACAACCAAGGTCTTCAGGTGACCAAGCAGCTCAAGTTTC	503
Db	421	CGCAAGGCCATCGGGAGATGACAACCAAGGTCTTCAGGTGACCAAGCAGCTCAAGTTTC	480
OY	504	ATCAAGATGTCTGTGCGCGGTGTGCGCGAGACGAGAGCAAGATCTAATCTGTGTGAAG	563
Db	481	ATCAAGATGTCTGTGCGCGGTGTGCGCGAGACGAGAGCAAGATCTAATCTGTGTGAAG	540
OY	564	GAGGAGAAAGCGTACGCGGACGCGCAAGCTGTCTGGCAAGGCGCGGGGGCAAGCTGAGC	623
Db	541	GAGGAGAAAGCGTACGCGGACGCGCAAGCTGTCTGGCAAGGCGCGGGGGCAAGCTGAGC	600
OY	624	ATGCCCAAGACGAGGCTGCCAATGGCTTGATGGCCGATACCTGGCGCAAGCGGCTTG	683
Db	601	ATGCCCAAGACGAGGCTGCCAATGGCTTGATGGCCGATACCTGGCGCAAGCGGCTTG	660
OY	684	GCCCGTGTTCATCGGCATCAACGACCTGGAGAAAGAGGGCGCTTGTGTACTCTGAC	743
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: RESULT 12
: US-09-989-721-356
: Sequence 356, Application US/09989721
: Patent No. US20020142961A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertsitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730PIC55
: CURRENT APPLICATION NUMBER: US/09/989,721
: CURRENT FILING DATE: 2001-11-19
: PRIOR APPLICATION NUMBER: 60/049787

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PRIOR APPLICATION NUMBER:	60/089444
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
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QY 144 CTGCTGCATCTGACATCTCTCAGCGCGCTGCGATGACGCTGCTGCTGCTGCAATCTCTC 203  
DB 121 CTGCTGCATCTGACATCTCTCAGCGCGCTGCGATGACGCTGCTGCTGCTGCAATCTCTC 180  
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QY 324 GTGGCTGCTCAATGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAAGAGATTCCGGT 383  
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DB 721 CACTCCCCCAGGCGGAGCTTCAACAGAGTGGGAGCGGCTGAGGCCCAAGATGCCATGAGC 780  
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; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zhen  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787

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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
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;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.2%; Score 1230; DB 9; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GGAGGGGAGGAGCGCCGCTTGGCTAGCGGCTGCTGAGAGTTGGTCTCTGCTGG 83  
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; Sequence 356, Application US/09989293A  
; Patent No. US20020177164A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geisler, Hanspeter  
; APPLICANT: Gerlt, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C66  
; CURRENT APPLICATION NUMBER: US/09/989, 293A  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787

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Query Match      98.2%; Score 1230; DB 9; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      601 ATGCCCAAGGAGAGAGCTGGCCCAATGGCCGAGAGCCGCACTACTGCGGCAACCGGCGTG 660
QY      684 GCCCGTGTCTTATCGGCACTCAACGACTGAGAGAGAGGCGGCTTGTGTACTGTGAC 743
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QY      744 CACTCCCCCATGGGAGACCTTCAACAGTGGCGACGCGGTGAGCCCAACATATGCTTACGAC 803
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QY      804 GAGAGAGACTGCTGAGAGATGGTGGCTCGGCGCGCTGGAACGAGCTGGCCTGCACACC 863
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QY      864 ACCATGTACTTCAATGTGTGATTTGACAGAGAAACATGTAGCCTCAGGCTGGGGCTGC 923
DB      841 ACCATGTACTTCAATGTGTGATTTGACAGAGAAACATGTAGCCTCAGGCTGGGGCTGC 900
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DB      961 CAGCAGGAGACTGTCCCTCTGTGAAGGGTGAAGGCTCACTGATGAGAGGCTGTGTCT 1020
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; Sequence 356, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colijn K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      84 CTCAGAGTGGGGGAAATCTGGCCCTGGTGGGCGTTCTAATCAGCGCTTGCCCTGCA 143
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DB      241 GGAAGAGTGGGCGCCAGCGGAGAAAGGAGCATGGGGGCAAAAGGAGCAGAAAGCACT 300
QY      324 GTGGGTCTCATAGAAATTTGTTCCCATTTGGCTCTAAAGTGAAGAAAGATTCGGGT 383
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QY      384 GACATAGACCCCTGGTCTTAATGAGAACCAAGCCTCCATGTGAGTGACAGCACTG 443
DB      361 GACATAGACCCCTGGTCTTAATGAGAACCAAGCCTCCATGTGAGTGACAGCACTG 420
QY      444 CGCAAGGCCATGGGGAGATGACAAACAGGTCTCTCACTGACCAAGGCTCAAGTTTC 503
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DB      481 ATCAAGATGTGTGCGCGGTGTGCGAGACGAGACGAGAGCAATCTACTGCTGTGAAG 540
QY      564 GAGAGAACCGCTACCGGAGCGCCAGCTGTCTTCCAGGGCTCGCGGGGCAAGCTGAGC 623
DB      541 GAGAGAACCGCTACCGGAGCGCCAGCTGTCTTCCAGGGCTCGCGGGGCAAGCTGAGC 600
QY      624 ATGCCCAAGAGAGAGCTGCAATGGCTGATGCGCGCATACCTGCGCGCAAGCGGCTTG 683
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DB      661 GCCCGTCTTCTCATCGGCATCAACGACCTGAGAAAGAGGCGCTTCTGTACTGTGAC 720
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QY      744 CACTCCCATGCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACAATGCTTACGAC 803
DB      721 CACTCCCATGCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACAATGCTTACGAC 780
QY      804 GAGAGAGCTGCGTGAAGATGTGGCTCGGGCGGCTTGAAACGACGTGGCTGCGCACAC 863
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QY      1104 TGAAGAGCAGAGTTTCTTACTGTAATTTGAGCCCAATGTCAATTAATTAATTAAC 1163
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QY      1164 CAGATTTGCTTTCATTAAGCTTGTGCTTGTCAAGCTTAACAATTAATCTTTAAG 1223
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Job time : 4172 secs

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QY	301	GGGACAAAGAGACAGAAAGGCGAGTGGGGTGTCTATGAAAAATTGGTCCCATTTGGCTCTA	360
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QY	421	TCCCATGTGAAGTGACGCCAGCTTGCAGAGGCCATCGGGGAGATGAGCAACAGGTCTCTC	480
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QY	481	AGCTACACGAGCGATCAAGTTCAATCAAGAAATGCTGCGCGGTGGCGCGAGACGGAGA	540
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QY	541	GCAAGATCTACTCTGTGTGAGAGAGAGAAAGCGCTACCGAGACGCCAGCTGCTCTGC	600
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QY	601	AGGGCGGGGGGGGACGCTGAGACATGCCCCAAGAGAGAGGCTGCCAATGGCTGATGGCCG	660
Db	603	AGGGCGGGGGGGGACGCTGAGACATGCCCCAAGAGAGAGGCTGCCAATGGCTGATGGCCG	662
QY	661	CATACCTGGCGCAACCGCGCTGCGCCCGTCTTATCGGACATCAACGACTCTGAGAAAG	720
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Db	723	AGGGCGCTTGTGTGTAATCTGTGACCACTCCCCATGCGGACCTTCAACAAGTGGCCGACGG	782
QY	781	GTCAGCCCAACAAATGCTTACGACGAGAGAGAACTGGTGGAGATGGTGGCGTGGCGCGCT	840
Db	783	GTCAGCCCAACAAATGCTTACGACGAGAGAGAACTGGTGGAGATGGTGGCGTGGCGCGCT	842
QY	841	GGAAAGACGTGGCCTGCCACACCAACATGTACTTATGTGTGAGTTTGAACAAGAAACA	900
Db	843	GGAAAGACGTGGCCTGCCACACCAACATGTACTTATGTGTGAGTTTGAACAAGAAACA	902
QY	901	TGTGAGCCTCAGGCTGGGGGTGCCCATTTGGGGGCCCAATGTCCCTGAGGGTGGCAG	960
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QY	961	GGACAGAGCCCAAGACATGTGTGCCAGCGAGGGAGCTGTCCTCTGTGAAGGGTGAAGGCT	1020
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QY	1141	AATGCATTAATGTAATTAATTAATCCAGAAATGCTCTGCATTAAGACTGTGGCTTTGTC	1200
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LOCUS		full-length cDNA clone GSDC024YP19 of Neuroblastoma Cot	
DEFINITION		25-normalized of Homo sapiens (human).	
ACCESSION		CR604552.1	GI:5048535
VERSION		CR604552.1	GI:5048535
KEYWORDS		HTC; CNSLT_cDNA.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE		1 (bases 1 to 1252)	
JOURNAL		Li,W.B., Gruber,C., Jeehee,J. and Polayes,D.	
REMARK		Full-length cDNA libraries and normalization	
REFERENCE		Unpublished	
AUTHORS		Contact : Feng Liang Email : fliang@lifetech.com URL :	
TITLE		http://fulllength.invitrogen.com/Invitrogen Corporation 1600	
JOURNAL		Parady Avenue	
REMARK		2 (bases 1 to 1252)	
REFERENCE		Genoscope.	
AUTHORS		Direct Submision	
TITLE		Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :	
JOURNAL		BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr	
COMMENT		- Web : www.genoscope.cns.fr)	
FEATURES		1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime	
SOURCE		end enriched, double-strand cDNA was digested with Not I and cloned	
		into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library	
		was normalized. Library was constructed by Life Technologies, a	
		division of Invitrogen.	
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Query Match		98.8%; Score 1238; DB 3; Length 1252;	
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Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	121	TAAACACCTGGGCTTCTCTGCACTGGTGCATCTGGACATCTCTCAGCCGGCTGGCGATG	180
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QY	181	ACGCTGCTCTGTGTCAGATCTCTGTCCCTTCAAGGGGATGCGGAGAGAGAGAGAG	240
Db	195	ACGCTGCTCTGTGTCAGATCTCTGTCCCTTCAAGGGGATGCGGAGAGAGAGAGAGAG	254
QY	241	ACAAAGGCGCCCGCGAGCGGCTGGAAGAATCGGCCCCACGGAGAAAAAGAGACATGG	300
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QY 541 GCAAGATCTACTGCTGTGTAAGAGAGAAACGCTACGCGGACCCGAGCTGTCTCTCC 600
Db 555 GCAAGATCTACTGCTGTGTAAGAGAGAAACGCTACGCGGACCCGAGCTGTCTCTCC 614
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Db 675 CATACCTGGCGGACACCGGCTGCGGCTGTCTTCAATGGGATCAACGACCTGGAGAAAG 734
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RESULT 3
CRS99770 1150 bp mRNA linear HTC 21-JUL-2004
LOCUS Full-length cDNA clone CS0DC018YD07 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CRS99770
VERSION CRS99770.1 GI:50480577
KEYWORDS HTC; cnsLUT_cDNA.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1150)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
location/Qualifiers
1..1150
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Beet Local Similarity 94.1%; Pred. No. 3.9e-257;
Matches 1143; Conservative 0; Mismatches 0; Indels 72; Gaps 1;
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Db 8 GGGGGCAGTGTCTTCGCGGGGACAGCGGCGAGAGAGCCCGCTTGGCTGCGCGTCT 67
QY 61 CAGAGTTGTGTGTCTGCTGCGCTCAGATGAGGGGAAATCTGGCCCTGTGGGCGTTC 120
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QY 241 ACAAAAGGCGCCCGGAGAGGCTGGAAGATCGGCGCCACAGGAGAAAAAGAGACATGG 300
Db 223 -----AAAGAGACATGG 235
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Db	776	GGAAAGAGCTGGCTCGGACCAACCAACCATGTACTATGTGTGATTTGACAAAGAGAAACA	835
QY	901	TGTGAGCTTCAGGCTGGGGCTGGCCATTGGGGGGCCCCACATGTCTCTGCAAGGTTGGACG	960
Db	836	TGTGAGCTTCAGGCTGGGGCTGGCCATTGGGGGGCCCCACATGTCTCTGCAAGGTTGGACG	895
QY	961	GGACAGAGCCCGACGACCATGAGTCCAGCCAGAGGAGCTGTCCCTCTGTGAAGGGTGGAGGCT	1020
Db	896	GGACAGAGCCCGACGACCATGAGTCCAGCCAGAGGAGCTGTCCCTCTGTGAAGGGTGGAGGCT	955
QY	1021	CACTGAGTGAAGGGGCTGTGTCTTAACCTGAGAAATGGCCCTATGCTTAAGAGAAATGA	1080
Db	956	CACTGAGTGAAGGGGCTGTGTGTCTTAACCTGAGAAATGGCCCTATGCTTAAGAGAAATGA	1015
QY	1081	AAGTGTCTCTGGGGGCTGTCTCTGGAAGAAGAGAGTTCAATTAACCTGATTTGAGCCCC	1140
Db	1016	AAGTGTCTCTGGGGGCTGTCTCTGGAAGAAGAGAGTTCAATTAACCTGATTTGAGCCCC	1075
QY	1141	AATGTCATTATGTATTAATTATACCGAAGATGCTCTTCCATTAAGCTTGGCTTTGTCCA	1200
Db	1076	AATGTCATTATGTATTAATTATACCGAAGATGCTCTTCCATTAAGCTTGGCTTTGTCCA	1135
QY	1201	AGCTTATCAATATAAA 1215	
Db	1136	AGCTTATCAATATAAA 1150	
RESULT 4			
LOCUS	BX427124	1083 bp	mRNA linear EST 04-MAY-2004
DEFINITION	BX427124 Homo sapiens FETAL LIVER Homo sapiens cDNA clone		
ACCESSION	CSDDM008Y118 5-PRIME, mRNA sequence.		
VERSION	BX427124		
KEYWORDS	BX427124.2 GI:47002248		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Li, W.B., Gruber, C., Jesssee, J., and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
	On May 15, 2003 this sequence version replaced gi:30774621.		

Contact: Genoscope - Centre National de Séquençage  
BP 151 91006 EVRY cedex - France  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-1050(dT) primer. Five primers  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.  
 This sequence belongs to sequence cluster 1719.f  
 For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?c=CSOAM008DF09QPI&c=1719.f>  
 location/Qualifiers  
 1. 1083

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/clone lib="Homo sapiens FETAL LIVER"
/note=Torgan: liver; Vector: pCMVSport_6; 1st strand cDNA
was primed with a NotI-Oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSport 6
vector. Library was not normalized."

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## ORIGIN

Query Match	75.2%;	Score 942.2;	DB 5;	Length 1083;
Best Local Similarity	97.3%;	Pred. No. 4,3e-227;		
Matches 966;	Conservative 11;	Mismatches 14;	Indels 2;	Gaps 2

Qy	1	GGGGGAGAGTCTCTGGGGGACAGGAGAGGGACAGAGCCCGGTGCTAGAGCGGTCT	60
Dp	3	GGGGGAGAGTCTCTGCGGGGACAGGAGAGGGACAGAGCCCGGTGCTAGAGCGGTCT	62
Qy	61	CAGAGTTGATGTCCTGCTGCGCTCAGAGATGAGGGGAAATCTGGCCCTGATGGCGTTT	120
Dp	63	CAGAGTTGATGTCCTGCTGCGCTCAGAGATGAGGGGAAATCTGGCCCTGATGGCGTTT	122
Qy	121	TATCAGCGTGGCGCTTCCTGTCACGTGCGCATCTGCAATCTCTACCGCGCTGGCGATG	180
Dp	123	TATCAGCGTGGCGCTTCCTGTCACGTGCGCATCTGCAATCTCTACCGCGCTGGCGATG	182
Qy	181	ACGCTGCTCTGTGACAGATCTCTGTCCTGCTCAAAAGGGATGCGGAGAGAGAGGAG	240
Dp	183	ACGCTGCTCTGTGACAGATCTCTGTCCTGCTCAAAAGGGATGCGGAGAGAGAGGAG	242
Qy	241	ACAAAGGCGCGCGCGGAGCGGCTGGAAAGTGGCGCCCAAGGAGAAAGAGAGACATGG	300
Dp	243	ACAAAGGCGCGCGCGGAGCGGCTGGAAAGTGGCGCCCAAGGAGAAAGAGAGACATGG	302
Qy	301	GGGACAAAGAGACAGAAAGGACAGTGTGGGTCTCTCATGGAATAATGGTCCCATTTGGCTTA	360
Dp	303	GGGACAAAGAGACAGAAAGGACAGTGTGGGTCTCTCATGGAATAATGGTCCCATTTGGCTTA	362
Qy	361	AAGGTGAGAAAGGAATTTCCGGTGCATATGGAACCCCTGGTCTTAATGGAAGAACAGGCC	420
Dp	363	AAGGTGAGAAAGGAATTTCCGGTGCATATGGAACCCCTGGTCTTAATGGAAGAACAGGCC	422
Qy	421	TCCCATGTGATGTCAGCGACGATGCGCAAGGAGCATGCGGGAGATGGAACAACAGATCTCTC	480
Dp	423	TCCCATGTGATGTCAGCGACGATGCGCAAGGAGCATGCGGGAGATGGAACAACAGATCTCTC	482
Qy	481	AGTGTACACGAGAGCTCAAATTCATCAAAGATGCTGTGTCGCCGTGTGTCGGAACGGAAG	540
Dp	483	AGTGTACACGAGAGCTCAAATTCATCAAAGATGCTGTGTCGCCGTGTGTCGGAACGGAAG	542
Qy	541	GCAAGATCTACCTGTGTGTGAAGAGGAGAGAGCCCTACGCGAGACGCCCACTGTCTGGC	600
Dp	543	GCAAGATCTACCTGTGTGTGAAGAGGAGAGAGCCCTACGCGAGACGCCCACTGTCTGGC	602
Qy	601	AGGGCGCGGGGGACGCTGAGCATGCCCAAAGACGAGGCTTGCCCAATGACTGATGGCG	660
Dp	603	AGGGCGCGGGGGACGCTGAGCATGCCCAAAGACGAGGCTTGCCCAATGACTGATGGCG	662
Qy	661	CATTACCTGGCGCAACGCGGCGGTGGCCCGTGTCTTCAATCGGATCTCAACGACTGGAAGG	720
Dp	663	CATTACCTGGCGCAACGCGGCGGTGGCCCGTGTCTTCAATCGGATCTCAACGACTGGAAGG	721
Qy	721	AGGGCGCGCTTGTGTACTGTAGCACTCCCATGCGAGACCTTCACAACTGAGCGACG	780

Db 722 AGGGGCGCTTCTGTAAGCTTGAACCACTCCCATCGGACCTTCAACAAGTGGGSMGG 781  
Qy 781 GTGAGCCCAACATGCTTACGACGAGAGAGAGTCTGCTGAGATGGTGGCTTGGCGGCT 840  
Db 782 TGGAGCCCAACATGCTTACGACGAGAGAGTCTGCTGAGATGGTGGCTTGGCGGCT 841  
Qy 841 GGAAGAGTGGCTGCTGCAACCAACCATGTAATTTATGTGATGATTTTAAAGAGAA 900  
Db 842 GGAAGAGTGGCTGCTGCAACCAACCATGTAATTTATGTGATGATTTTAAAGAGAA 901  
Qy 901 TGTGAGCTTCAAGCTGAGGCT-GCCCATTTGGGGGCCCAATGTCCTGACAGGTTGGCA 959  
Db 902 TGTGAGCTTCAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 961  
Qy 960 GGGACAGAGCCCAACATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 992  
Db 962 GGGACAGAGCCCAACATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 994

RESULT 5  
LOCUS BX333394 1078 bp mRNA linear EST 07-APR-2004  
DEFINITION BX333394 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
ACCESSION BX333394  
VERSION BX333394.2 GI:46262347  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1078)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 1, 2003 this sequence version replaced gi:30308204.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1719.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?cs=CS0DC024CH10QPI&c=1719.f.

FEATURES  
Source  
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Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DC024YP19"  
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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  
ORIGIN  
Query Match 75.1%; Score 941.2; DB 5; Length 1078;  
Best Local Similarity 98.0%; Pred. No. 7.8e-227;  
Matches 1013; Conservative 3; Mismatches 11; Indels 7; Gaps 6;  
Qy 1 GGGGCGAGTGTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 60  
Db 15 GGGGCGAGTGTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 74  
Qy 61 GAGGAGTGTGTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 120

Db 75 CAGGAGTGTGTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 134  
Qy 121 TAATCAGCTTGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
Db 135 TAATCAGCTTGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194  
Qy 181 AGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
Db 195 AGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254  
Qy 241 ACAAAGCGCCCGCGAGCGGCTGGAAGTGGCCCGCGCGGAGAAAGAGACATGG 300  
Db 255 ACAAAGCGCCCGCGAGCGGCTGGAAGTGGCCCGCGCGGAGAAAGAGACATGG 314  
Qy 301 GGGACAAAGGACAAAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Db 315 GGGACAAAGGACAAAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374  
Qy 361 AAGGTGAGAAAGGAGATTCCGGTGAATAGAACCCCGCTGCTTAAATGAGAACAGG 420  
Db 375 AAGGTGAGAAAGGAGATTCCGGTGAATAGAACCCCGCTGCTTAAATGAGAACAGG 434  
Qy 421 TCCCATGTGAGTGAAGCGAGCTGCGCAAGGCGCATCGGAGATGAGACCAAGTCTTC 480  
Db 435 TCCCATGTGAGTGAAGCGAGCTGCGCAAGGCGCATCGGAGATGAGACCAAGTCTTC 494  
Qy 481 AGCTGACCAAGGAGCTCAAGTTTCAATCAAGATGCTGCTGCTGCTGCTGCTGCTG 540  
Db 495 AGCTGACCAAGGAGCTCAAGTTTCAATCAAGATGCTGCTGCTGCTGCTGCTGCTG 554  
Qy 541 GCAAGATCTACTCTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599  
Db 555 GCAAGATCTACTCTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 614  
Qy 600 CAGGCGCGCGGCGGCGAGCTGAGATGCGCAAGAGAGAGAGAGAGAGAGAGAGAG 659  
Db 615 CAGGCGCGCGGCGGCGAGCTGAGATGCGCAAGAGAGAGAGAGAGAGAGAGAGAG 674  
Qy 660 GCATACCTGCGGCGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719  
Db 675 GCATACCTGCGGCGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733  
Qy 720 GAGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779  
Db 734 GAGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792  
Qy 780 GGTGAGCCCAACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839  
Db 793 GGTGAGCCCAACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 852  
Qy 840 TGAACGAGCTGCGCTGCGACACCAACATGTAATGTGTGAGTTGACAAAGAGAG 899  
Db 853 TGAACGAGCTGCGCTGCGACACCAACATGTAATGTGTGAGTTGACAAAGAGAG 912  
Qy 900 ATGTGAGCTGAGCTGAGGCTGCGACACCAACATGTAATGTGTGAGTTGACAAAGAGAG 959  
Db 913 ATGTGAGCTGAGCTGAGGCTGCGACACCAACATGTAATGTGTGAGTTGACAAAGAGAG 972  
Qy 960 GGGACAGAGCCCAACATGCTGAGGCTGCGACACCAACATGTAATGTGTGAGTTGACAAAGAGAG 1019  
Db 973 GGGACAGAGCCCAACATGCTGAGGCTGCGACACCAACATGTAATGTGTGAGTTGACAAAGAGAG 1028

ORIGIN  
Query Match 102.0%; Score 1020.0; DB 1020; Length 1020;  
Best Local Similarity 100.0%; Pred. No. 1.0e-227;  
Matches 1029; Conservative 1029; Mismatches 0; Indels 0; Gaps 0;  
Qy 1020 TCACTGAGTAGAGG 1033  
Db 1029 TCACTGAGTAGAGG 1042

RESULT 6  
LOCUS BX394893 1095 bp mRNA linear EST 01-MAY-2004  
DEFINITION BX394893 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
ACCESSION BX394893  
CDNA clone CS0DC024YP19 3-PRIME, mRNA sequence.

VERSION BX394893.2 GI:46921106  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1095)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 13, 2003 this sequence version replaced gi:30628356.  
 Contact: Genoscope

Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by life technologies, a  
 division of invitrogen. This sequence belongs to sequence cluster  
 1719.f

For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?cs=CS0DC024CH1ONP1&c=1719.f.

## FEATURES

source

Location/Qualifiers

1..1095

/organism="Homo sapiens"

/mol\_type="mRNA"

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/issue\_type="NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. This sequence belongs to sequence cluster

1719.f

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## ORIGIN

Query Match 74.0%; Score 927.4; DB 5; Length 1095;

Best Local Similarity 97.5%; Pred. No. 2,4e-223;

Matches 1015; Conservative 10; Mismatches 7; Indels 9; Gaps 8;

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 1033 GACATCCCTCAGCGGCTGGGATGACGCTGCTGTCAGATCCTGCTCCCTGAGCTCA 976  
 217 AAGGGGATGCGGAG 275  
 975 AAGGGGATGCGGAG 916  
 276 CCCACGGGAG 335  
 915 CCCACGGGAG 856  
 336 GGAAGAAATTTGCTCCATTTGCTCTTAAGGTGAAGAGAGAGAGAGAGAGAGAGAG 395  
 855 GGAAGAAATTTGCTCCATTTGCTCTTAAGGTGAAGAGAGAGAGAGAGAGAGAGAG 797  
 396 CTTGCTCTTAATGAG 455  
 796 CTTGCTCTTAATGAG 738  
 456 GGGGAGATGAG 515  
 737 GGGGAGATGAG 678  
 516 GTCCGCGGTGTGCGGAG 575  
 677 GTCCGCGGTGTGCGGAG 620  
 576 TACGCGAG 635  
 619 TACGCGAG 560

QY 636 GAGGCTCCCAATGAGCTGATGAGCCGCATACCTGAGCGGAGAGAGAGAGAGAGAGAG 695  
 DB 559 GAGGCTCCCAAT-GCCGATGAGCTGCAATGCTGAGCGGAGAGAGAGAGAGAGAGAG 501  
 QY 696 ATGGGATCAAG 755  
 DB 500 ATGGGATCAAG 441  
 QY 756 CGAGCTTCAAG 815  
 DB 440 CGAGCTTCAAG 381  
 QY 816 GTGAGATGAGTGGCTCCGCGGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 875  
 DB 380 GTGAGATGAGTGGCTCCGCGGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 321  
 QY 876 ATGATGAGATTTGAAG 935  
 DB 320 ATGATGAGATTTGAAG 261  
 QY 936 CCAATGTCCTTGAAG 995  
 DB 260 CCAATGTCCTTGAAG 201  
 QY 996 TGTCCCTGTGAG 1055  
 DB 200 TGTCCCTGTGAG 141  
 QY 1056 TGCCCTGTGAG 1115  
 DB 140 TGCCCTGTGAG 81  
 QY 1116 GTTTCATTTACCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1175  
 DB 80 GTTTCATTTACCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 22  
 QY 1176 TCCATTAAGCTTGCTGCTTG 1196  
 DB 21 TCCATTAAGCTTGCTGCTTG 1

## RESULT 7

BUI47034

## LOCUS

BUI47034

## DEFINITION

BUI47034

## ACCESSION

BUI47034

## VERSION

BUI47034.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens

## ORGANISM

Homo sapiens (human)

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 894)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-rt@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LMNL at:

http://image.llnl.gov

Plate: LLM2532 row: i column: 13

High quality sequence stop: 621.

Location/Qualifiers

1..894

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

## FEATURES

source



## ORIGIN

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QY	79	CTGCGCTCAGGATGAGGGGGAACTTGCCCTGTGTGGCGTTCTAATCAGCTGGCGTTCC	138
Db	61	CTGGCGCTCAGGATGAGGGGGAACTTGCCCTGTGTGGCGTTCTAATCAGCTGGCGTTCC	120
QY	139	TGTCACTGCTGTGCATCTGGACATCTCAGCCGGCTGGCGATGACGCTGTCTCTGTGCGA	198
Db	121	TGTCACTGCTGTGCATCTGGACATCTCAGCCGGCTGGCGATGACGCTGTCTCTGTGCGA	180
QY	199	TCCTGTGCTCCGGGCTCAAAAGGGGATGGGGGAGAGAAAGGAGACAAAGGCGCCCCGAC	258
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QY	379	CCGGTGAATAGAACCCCTGTGCTTAATGAGAAACAGGCTCCCATTTGATGTGACGCC	438
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QY	499	AGTTCATCAAGAAATCTGTCCGCGGTGTGCGGAGACGAGAGCAAGATCTCATGCTGG	558
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QY	619	TGAGCATGCCCAAGGACGAGGCTGCCAATGGCTGTGATGGCGGCATTACTTGGCGCAAGCCG	678
Db	601	TGAGCATGCCCAAGGACGAGGCTGCCAATGGCTGTGATGGCGGCATTACTTGGCGCAAGCCG	660
QY	679	GCTGGGCGGTGTCTTCAATCGGATCAACAGACTGAGAGAGAGGGCGGCTTGCTGCTACT	738
Db	661	GCTGGGCGGTGTCTTCAATCGGATCAACAGACTGAGAGAGAGGGCGGCTTGCTGCTACT	720
QY	739	CTGACCACTCCCCCATGGGACCTTCAACAAGTGGCGCAGCGGTAGGCCCAACAATGCTCT	798
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QY	799	ACGACGAGAGAGACTGGCTGAGATGTGGCTTCGGGCGGCTTGAAACGACGTGGCTGCTC	858

RESULT 8  
BX394624/C

**VERSION**  
**KEYWORDS**

**SOURCE ORGANISM**

## REFERENCE

Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France

Email: [seger@genoscope.cns.fr](mailto:seger@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1719.f

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?b=CS0DC018CB04NP1&c=1719.f>

## FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC018YD07"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_1lb="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-01:60 (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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**ORIGIN**

Query Match	69.5%;	Score 871;	DB 5;	Length 1071;
Best Local Similarly	88.8%;	Pred. No. 4.4e-209;		
Matches 1010;	Conservative 14;	Mismatches 37;	Indels 77;	Gaps 5.

Qy

db 1061 CYCCCGCS(CAGGATRAAGGGGASTYTGSCACTGK-GCGGTTCTAATCACCCTGGCTCC 1003

138 CTGTCACTGCTGCATCTGACATCTCAAGCCGGCTGGCGATGACGCCCTGTGTGAG 197

Db 1002 CTGTACAGCTGCATCTGACATCCTCAGCCGGCTGGGATRACGCTGCTGTGCAG 943

198 ATCTCGTCCCTTGCCCTCAAGGGGATGCGGGAGAGAAGGAGACAAGGCGCCCGGGA 257

Db 942 ATCTCGTCCCTGGCTCAAAGGAGACAT----- 914

258 CGGCTGGAAGAGTCGGCCCCACGGGAGAAAAGAGACATGGGGACAAGACAGAAA 317

Db 913 -----GGGGCAAAAGAACGAAA 896

318 GGCAGTGTGGGTCGTCATGMAAAATTGGTCCATTGGCTTAAGGTGAAGAAGAGAT 377

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 QY 918 GGCCTGGCCATTTGG 977  
 Db 297 GGCCTGGCCATTTGG 238  
 QY 978 TGTGTCCAGCAGGAGGCTGTCCCTGTGTGAAGGGTGAAGGCTCACTAGTGAAGAGGCTG 1037  
 Db 237 TGTGTCCAGCAGGAGGCTGTCCCTGTGTGAAGGGTGAAGGCTCACTAGTGAAGAGGCTG 178  
 QY 1038 TTTGTCTAACTGAGAAAATGAGCTTAAAGGAAAATGAAGATGTTCTTGGGGTGC 1097  
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 LOCUS BQ927000  
 DEFINITION AGENCOURT 8804355 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6377965  
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 ACCESSION BQ927000  
 VERSION BQ927000.1 GI:22342031  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (Bases 1 to 962)  
 NIH-MGC <http://mhc.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE

JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Straubeberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.llnl.gov>  
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 /clone\_lib="NIH\_MGC\_47"  
 /notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the Laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 64.5%; Score 808.8; DB 5; Length 962;  
 Best Local Similarity 93.3%; Pred. No. 2.3e-193;  
 Matches 898; Conservative 0; Mismatches 56; Indels 8; Gaps 5;  
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 Db 121 TGTCACTGCTCCATCTGGAACATCTCTCAGCGGCTGCGATGACGCTGTGTGCGAGA 180  
 QY 199 TCTGTGCTCCCTGGCTCAAGAGGGGATGCGGAGAGAGAGGAGCAAGAGCGCCCGGAGC 258  
 Db 181 TCTGTGCTCCCTGGCTCAAGAGGGGATGCGGAGAGAGAGGAGCAAGAGCGCCCGGAGC 240  
 QY 259 GGCCTGAGAGAGTGGCGCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 318  
 Db 241 GGCCTGAGAGAGTGGCGCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
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 Db 481 AGTTTATCAAGAAATGTGTGCGCGGTGTGCGGAGAGAGAGAGAGAGATTTACTGCTGG 540  
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Db 541 TGAAGAGAGAGAGCGCTTACGCGAGCGCCAGCTGTCTCTGCCAGGGCCGGCGGGGCGACGCG 600

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Db 601 TGAGCATGCCCAAGAGACGAGGCTGCGCAATGAGCTGATGAGCGCGCATACCTGGCGCAAGCCG 660

Qy 679 GCCTGGCCCCGTGTCTTTCATCGGCATCAAGACCTTGA--GAGAGGGGCGCCCTTGCTGT 735

Db 661 GCCTGGCCCCGTGTCTTTCATCGGCATCAAGACCTGNNAGAGAGGGGCGCCCTTGCTGT 720

Qy 736 ACTGACACACATCCCCCATGCGGACCTTCAAGAATGGCGGACGCGTGAAGCCCAACAATG 795

Db 721 ACTTGACACATCCCCCATGCGGACCTTCAAGAATGGCGGACGCGTGAAGCCCAACAATG 780

Qy 796 CCTACGACGAGGAGAGACTG-CGTGAGATGATGGACTCGGGGCGGCTGGAAACGACGTTGGCC 854

Db 781 CCTACGACGAGGAGAGACTGCTCTTGGAAATGATGGCTCGGGGCGGCTGGGAAACGACGTTGGCC 840

Qy 855 TGCCACACACACCATATCTTC--ATGTGTAGTTTGAACAAGAGAGACAATGTAGGCC--TC 910

Db 841 TGCCACACACACATATACCTTTCATATGGGGGAAATTGGAACAAGAGAGACAATGTAGGCCCTTC 900

Qy 911 AGGCTGGGAGCTGCCCCATTTGGGGGCCCCACATGTCCCTGCGAGGTTTGGACGGAGACAGAGCC 970

Db 901 AGCTGGGGCCGCGCCCATATGGGGGCGCCATATGAGCCCTTTGAAAGGTTTGGACGAGGAAC 960

Qy 971 CA 972

Db 961 AA 962

RESULT 10	
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LOCUS	BQ069775 962 bp mRNA linear EST 02-APR-2002
DEFINITION	AGENCOURT 7054486 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5922062 5' mRNA sequence.

ACCESSION	BQ069775
VERSION	BQ069775.1
KEYWORDS	GI:19898821
SOURCE	EST.
ORGANISM	<i>Homo sapiens</i> (human)
REFERENCE	<i>Homo sapiens</i>
AUTHORS	Emura/Oda; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 362)
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.

Email: [CSABbs-remail.nih.gov](mailto:CSABbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: L12CM2088 row: f column: 15  
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 Location/Qualifiers  
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/clone_1b="NH MGC 47"
/notes="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACTGG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

```

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

[illegible]

LOCUS	969 bp	MRNA	linear	EST 04-MAY-2004
DEFINITION	BX427123	Homo sapiens FETL LIVER	cdna	clone
ACCESSION	BX427123	CSDDM008Y118 3-PRIME,	mrna	sequence.
VERSION	BX427123	GI:47001340		
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1. (bases 1 to 969)			
TITLE	L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.			
JOURNAL	Full-length cDNA libraries and normalization			
COMMENT	Unpublished (2001)			
	On May 15, 2003 this sequence version replaced gi:30772637.			
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	BP 191 91006 EVRY cedex - France			
	Email: secrete@genoscope.cns.fr, Web : www.genoscope.cns.fr			
	1st strand cDNA was primed with a NotI-oligo(GT) primer. Five primers			
	end enriched, double-strand cDNA was digested with Not I and cloned			
	into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			
	was not normalized. Library was constructed by Life Technologies, a			
	division of Invitrogen.			
	This sequence belongs to sequence cluster 1719.f			
	For more information about this cluster, see			
	http://www.genoscope.cns.fr/cdna?s=CS0AN008DF09NP1&c=1719.f.			

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/notes="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dm) primer. Five prime end
enriched double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN	
Query Match	60.0%; Score 751.2; DB 5; Length 969;
Best Local Similarity	96.5%; Pred. No. 8.8e-179;
Matches 772; Conservative	14; Mismatches 12; Indels 2; Gaps 2

[illegible]

Db	587	AGACCTGCGTGAACATGGTGGCTCTCGGGCGGCTGGAACGACGATGGCTGGCACACCA	528
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Db	527	TGTACTTCATGTGTGAGTTTGACAAGAGAAACATGTGAGCTCAGAGCTGGGGCTGGCCAT	468
Oy	928	TGGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCGACCATGTGCTCCAGC	987
Db	467	TGGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCGACCATGTGTCCAGC	408
Oy	988	CAGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCATGTAGTAGAGGGCTGTGTTCTTAAC	1047
Db	407	CAGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCATGTAGTAGAGGGCTGTGTTCTTAAC	348
Oy	1048	TGAGAAATGGCCATGTCTTAAGAGGAAATGAAAGTCTCTGGGGTGCCTCTCTAA	1107
Db	347	TGAGAAATGGCCATGTCTTAAGAGGAAATGAAAGTCTCTGGGGTGCCTCTCTAA	288
Oy	1108	GAAACAGAGTTTCATTAAGCTGTATTTGAGCCCAATGTCATTATGTATTAATTAACCCAGA	1167
Db	287	GAAACAGAGTTTCATTAAGCTGTATTTGAGCCCAATGTCATTATGTATTAATTAACCCAGA	228
Oy	1168	ATTGCTCTTCATTAAGCTGTGTGCTTTGTCCAAAGCTATACATTAATCTTTAAGTAGT	1227
Db	227	ATTGCTCTTCATTAAGCTGTGTGCTTTGTCCAAAGCTATACATTAATCTTTAAGTAGT	168
Oy	1228	GCAGTAGTTAAGTCCAAAA 1247	
Db	167	GCAGTAGTTAAGTCCAAAA 148	

RESULT	12
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DEFINITION	BX394625 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC018YD07 5-PRIME, mRNA sequence.
ACCESSION	BX394625
VERSION	BX394625.2
KEYWORDS	EST. GI:46920154
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	BASES 1 TO 1015
Li, W. B., Gruber, C., Jesse, J. and Polajny, D.	
Full-length cDNA libraries and normalization	
Unpublished (2001)	
On May 13, 2003 this sequence version replaced g130628263	

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segruff@genoscope.cns.fr, web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primers  
enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalised. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1719.F

For more information about this cluster, see  
<http://www.genoscope.cns.fr/cda?n=CS0DDC018CB04QP1kc=1719.f>  
 Location/Qualifiers  
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 FEATURES  
 source

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/note="1st strand cDNA was primed with a NotI-oligo (dT)
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sites of the pCMVSPORT 6 vector. Library was normalized."

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/clone="IMAGE:4127454"  
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 /note="Organ: brain; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 54.9%; Score 687.4; DB 2; Length 788;  
 Best Local Similarity 96.7%; Pred. No. 1.1e-162;  
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 61 TGCCCTGCGCTCAGAGTGGGAGGAACTGGCCCTGGTGGGCGTTCTAATCAGCCCTG 120  
 136 TCCTGTCACTGCTGTCATCTGGACATCTCTCAGCCGCTGCGATGACCGCTGCTGTGC 195  
 121 TCCTGTCACTGCTGTCATCTGGACATCTCTCAGCCGCTGCGATGACCGCTGCTGTGC 180  
 196 AGATCTCTGCTGCTGCTCCTCAAAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCG 255  
 181 AGATCTCTGCTGCTGCTCCTCAAAAGGAGATGCGGAGAGAAAGGAGACAAAGCGCCCG 240  
 256 GACGCGCTGGAAGAGTGGGCGCCAGCGGAGAAAGAGACATGGGAGGACAAAGAGACGA 315  
 241 GACGCGCTGGAAGAGTGGGCGCCAGCGGAGAAAGAGACATGGGAGGAGAAAGAGACGA 300  
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 601 ACGGAGAGATGCGCAAGGAGTACGAGGCTGCGCAATGGCGTATGGCGGACATCTGAGCGCA 660  
 674 AGCGGCGCTGCGCGGTGTCTTCTATC-GGATCAACGAGCTGAGAA-GAGAGGCGCGCTTC 731  
 661 AGCGGCGCTGCGCGGTGTCTTCTATCGGGCATCAACGAGCTGAGAAAGGAGGCGCGCTTC 720  
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 721 GTGTAACTGACCAATCCCGCATGCGGACCTTCAACAAAGTGGCGGAGG 769

RESULT 15  
 BF206254

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 DEFINITION 601869264.F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4098278 5',  
 mRNA sequence.  
 ACCESSION BF206254  
 VERSION BF206254.1 GI:11099840  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 672)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgsb@rockefeller.edu  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: LNCM964 row: 0 column: 15  
 High quality sequence stop: 670.  
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## ORIGIN

Query Match 52.1%; Score 653.2; DB 2; Length 672;  
 Best Local Similarity 99.4%; Pred. No. 5e-154;  
 Matches 666; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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 1 GCGGGCCAGGACGCGGAGAGCGCCCGTTCAGGCGCTCAGAGTGGTCC 60  
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 61 TGCCCTGCGCTCAGAGTGGGAGGAACTGGCCCTGGTGGGCGTTCTAATCAGCCCTG 120  
 136 TCCTGTCACTGCTGTCATCTGGACATCTCTCAGCCGCTGCGATGACCGCTGCTGTGC 195  
 121 TCCTGTCACTGCTGTCATCTGGACATCTCTCAGCCGCTGCGATGACCGCTGCTGTGC 180  
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 316 AAGGAGTGTGGGTGCTCATGAGAAATTTGGTCCATTGGCTCTAAGGTGAAAGAGAG 375  
 301 AAGGAGTGTGGGTGCTCATGAGAAATTTGGTCCATTGGCTCTAAGGTGAAAGAGAG 360  
 376 ATTCGGTGAACATAGAGACCCCTGCTCTAATGAGAAACAGGCGCTCCCATGTAGTCA 435

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Db      361 ATTCCGATGACATAGAGACCCCTGGTCTCTAATGAGAAACAGGCTCCCATGTGATGCA 420
OY      436 GCCAGCTGCGCAAGGCCATCGGGAGATGACAAACAGGTCTTCAAGCTGACCAAGCAGC 495
Db      421 GCCAGCTGCGCAAGGCCATCGGGAGATGACAAACAGGTCTTCAAGCTGACCAAGCAGC 480
OY      496 TCAAGTTATCAAGATGCTGTCCGCGGTGTGCGCGAGACGAGAGCAAGATTACCTGC 555
Db      481 TCAAGTTATCAAGATGCTGTCCGCGGTGTGCGCGAGACGAGAGCAAGATTACCTGC 540
OY      556 TGGTGAAGAGAGAGAGCGCTACCGCGACGCCCAAGCTGTCTGCCAGGGCCGCGGGCA 615
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OY      616 CGCTGAGCATGCCCAAGACGAGGCTGCCAATGGCTTGTATGGCCGACATACCTGGGCGAG 675
Db      601 CGCTGAGCATGCCCAAGAGCGAGGCTGCCAATGGCTTGTATGGCCG-ATACCTGGGCGAG 659
OY      676 CCGGCTGGC 685
Db      660 CCGGCTGGC 669

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Search completed: December 16, 2004, 20:45:04  
 Job time : 6196 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 10:00:00 ; Search time 590 Seconds  
(without alignments)  
2411.175 Million cell updates/sec

Title: US-09-806-277A-6

Perfect score: 271  
Sequence: 1 MRGNLALGVLSLAFSL.....NDVACHTMFMCEPDKENM 271

Scoring table:  
OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8266295

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

MODEL=frame+ p2n model -DEV=slp  
-Q=/sgn2.1/USPTO EP001\_P/US09806277/rnatc\_15122004\_101700\_29742/app\_query.fasta\_1.455  
-DB=N Geneseq 23Sep04 -QFMT=fastap -SUFFIX=Oligo.rng -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MTN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09806277\_QCGN\_1\_1\_885@rnatc\_15122004\_101700\_29742 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESUBSTR -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOC  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_23Sep04:\*

1: geneseqn1980s:\*\n2: geneseqn1990s:\*\n3: geneseqn2000s:\*\n4: geneseqn2001as:\*\n5: geneseqn2001bs:\*\n6: geneseqn2002as:\*\n7: geneseqn2002bs:\*\n8: geneseqn2003as:\*\n9: geneseqn2003bs:\*\n10: geneseqn2003cs:\*\n11: geneseqn2003ds:\*\n12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	271	100.0	813	6	ABA91201	ABA91201 Human col
2	271	100.0	1238	3	AA265084	AA265084 Membrane
3	271	100.0	1238	3	AAC58385	AAC58385 Human PRO
4	271	100.0	1238	5	AAFA4230	AAFA4230 Human PRO
5	271	100.0	1238	6	ABL88155	ABL88155 Human PRO
6	271	100.0	1238	6	ABL95644	ABL95644 Human ang

7	271	100.0	1238	8	ACA64399	ACA64399 Novel hum
8	271	100.0	1238	8	ABX80858	ABX80858 Human sec
9	271	100.0	1238	8	ACD44367	ACD44367 CDNA encs
10	271	100.0	1238	8	ABX79538	ABX79538 Human sec
11	271	100.0	1238	8	ACA93559	ACA93559 Novel hum
12	271	100.0	1238	8	ABX81241	ABX81241 Novel hum
13	271	100.0	1238	8	ACA93057	ACA93057 Novel hum
14	271	100.0	1238	8	ABX17141	ABX17141 Human PRO
15	271	100.0	1238	9	ACA67996	ACA67996 Novel hum
16	271	100.0	1238	9	ACA88445	ACA88445 Human sec
17	271	100.0	1238	9	ACD81952	ACD81952 CDNA encs
18	271	100.0	1238	9	ADA37867	ADA37867 Human CDN
19	271	100.0	1238	9	ADA21553	ADA21553 Human CDN
20	271	100.0	1238	9	ADA10340	ADA10340 Human CDN
21	271	100.0	1238	9	ADA17884	ADA17884 CDNA encs
22	271	100.0	1238	9	ADA27992	ADA27992 Human CDN
23	271	100.0	1238	9	ADA94572	ADA94572 Human CDN
24	271	100.0	1238	9	ADA38797	ADA38797 Human CDN
25	271	100.0	1238	9	ADA92918	ADA92918 Human CDN
26	271	100.0	1238	9	ACH65513	ACH65513 Human CDN
27	271	100.0	1238	9	ADA22479	ADA22479 Human CDN
28	271	100.0	1238	9	ACD39503	ACD39503 Human CDN
29	271	100.0	1238	9	ADA06645	ADA06645 Human sec
30	271	100.0	1238	9	ADA39338	ADA39338 Human CDN
31	271	100.0	1238	9	ADB96364	ADB96364 Human PRO
32	271	100.0	1238	10	ADC57836	ADC57836 Human PRO
33	271	100.0	1238	10	ADCS5200	ADCS5200 Human PRO
34	271	100.0	1238	10	ADC12067	ADC12067 Human CDN
35	271	100.0	1238	10	ADC65489	ADC65489 Human PRO
36	271	100.0	1238	10	ADC07544	ADC07544 Human CDN
37	271	100.0	1238	10	ADC11534	ADC11534 Human CDN
38	271	100.0	1238	10	ADC14656	ADC14656 Novel hum
39	271	100.0	1238	10	ADD08188	ADD08188 Novel hum
40	271	100.0	1238	10	ADC82013	ADC82013 Human PRO
41	271	100.0	1238	10	ADD07655	ADD07655 Novel hum
42	271	100.0	1238	10	ADC82546	ADC82546 Human PRO
43	271	100.0	1238	10	ADD10456	ADD10456 Human sec
44	271	100.0	1238	10	ADD08726	ADD08726 Novel hum
45	271	100.0	1238	10	ADD06975	ADD06975 Novel hum

## ALIGNMENTS

RESULT 1	ABA91201	standard; DNA; 813 BP.
ID	ABA91201	standard; DNA; 813 BP.
AC	ABA91201;	
XX		
DT	19-FEB-2002 (first entry)	
XX		
DE	Human collectin polynucleotide SEQ ID NO 45.	
XX		
KW	Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;	
KW	protein therapy; infection; de.	
OS	Homo sapiens.	
XX		
PN	WO200181401-A1.	
XX		
PD	01-NOV-2001.	
XX		
PF	23-APR-2001; 2001WO-JP003468.	
XX		
PR	21-APR-2000; 2000JP-00120358.	
XX		
PA	(FUSO ) FUSO PHARM IND LTD.	
XX		
PI	wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishii Y;	
XX		
DR	WPI; 2002-055345/07.	
XX		
PT	New collectin family proteins, designated CL-L2-1 and CL-L2-2, expressed	



PT in kidney and for treatment and prevention of bacterial and viral  
PT infections.

PS Clam 2, Page 121; 134pp; Japanese.

XX The invention relates to human collectin family proteins (CL-L2-1 and CL-  
CC L2-2, sequences given in the specification, ABB56407-ABB56411 and  
CC ABB56414-ABB56416), their derivatives and fragments and a related  
collectin (CL-L2) of mouse origin (ABB56412) and polynucleotides encoding  
CC all or part of the proteins. The proteins have antibacterial and virucide  
CC activity and are used for protein therapy and treatment, prevention and  
CC diagnosis of bacterial and viral infections. The present sequence is that  
CC of a collectin polynucleotide of the invention.

XX Sequence 813 BP; 183 A; 225 C; 271 G; 134 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	6,54e-263	Length:	813
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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DB:	6	Gaps:	0

US-09-806-277A-6 (1-271) x ABA91201 (1-813)

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DB 1 ATGAGGGGGAAATCTGGCCCTGATGGGCGCTTCAATCAAGCTTGGCCCTTCTCACTGCTG 60
OY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
DB 61 CCATCTGACATCTCCACGACCGGCGCATGACGCTCTCTGTGCAGATCTGCTCCCT 120
OY 41 GlyLeuLysGlyAspAlaGlyGlyLysGlyAspLysGlyAlaProGlyArgProGlyArg 60
DB 121 GGCCCTCAAAAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
OY 61 ValGlyProThrGlyLysLysGlyLysPheMetGlyAspLysGlyLysGlySerValGly 80
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OY 81 ArgHisGlyLysIleGlyProIleGlySerLysGlyLysGlyLysGlyAspSerGlyAspIle 100
DB 241 CGTCATGAGAAATTTGCTCCATTTGGCTCTAAAGGTGAGAGAGAGAGAGAGAGAGAGAG 300
OY 101 GlyProProGlyProAsnGlyGluProGlyLeuProCysGlyLysCysSerGlyLeuArgLys 120
DB 301 GGAGCCCTGCTGCTCTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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DB 361 GCCATTCGGGAGATGACACCAAGGTCTCTCAAGCTGACACAGAGCTCAAGTTATCAAG 420
OY 141 AsnAlaValAlaGlyValArgGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 160
DB 421 AATGCTGTGCGCGGTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
OY 161 LysArgGlyTyrAlaAspAlaGlnLeuSerCysGlnGlyLysGlyLysGlyLysGlyLys 180
DB 481 AAGGCTAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
OY 181 LysAspGlyLysAlaAsnGlyLysMetAlaAlaTyrLeuAlaGlnAlaGlyLysLysArg 200
DB 541 AAGGACAGAGGCTTCCATGCTGATGGCCCAATCTGAGGAGAGAGAGAGAGAGAGAGAG 600
OY 201 ValPheIleGlyLysAspLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 220
DB 601 GTCTTCAATCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
OY 221 ProMetArgThrPheAsnLysTyrArgSerGlyLysProAsnAsnAlaTyrArgGlyLys 240
DB 661 CCCATGGGAGACTTCAACAGTGGCGAGCGGTGAGGCCCAATGCTTCAAGAGAGAGAGAGAG 720
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OY 241 AspCysValGlyMetValAlaSerGlyLysTyrAsnAspValAlaCysHisThrThrMet 260
DB 721 GACTGCTGAGAGATGGTGGCTTGGGCGGCTGAGAACGATGGCTGCCACACCATCATG 780
OY 261 TyrPheMetCysGlyPheAspLysGlyLysMet 271
DB 781 TACTTCAATGTGATGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813
RESULT 2
AAZ65084
ID AAZ65084 standard; cDNA; 1238 BP.
XX
AC AAZ65084;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1182 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX Homo sapiens.
XX
PN WC9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WC-US012252.
XX
XX 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
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PR 12-JAN-1999; 99US-0115565P.  
  
XX (GETH ) GENENTECH INC.  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,  
PI Wood WJ, Yuan J;  
XX WPI; 2000-072883/06.  
DR P-PSDB; AAY66738.  
XX  
PT Membrane-bound proteins and related nucleotide sequences.  
XX  
XX Claim 2; Fig 251; 822pp; English.  
XX  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
SQ  
  
Alignment Scores:  
Pred. No.: 9,91e-263 Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Matchn: 100.00% Indels: 0  
DB: Gaps: 0  
  
US-09-806-277A-6 (1-271) x AA265084 (1-1238)  
  
QY 1 MetArgGlyAenLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeu 20  
DB 67 ATGAGGGGGAATCTGGCGCTGTGGCTTAAATCAAGCCCTGCTCTCACTGTG 126  
QY 21 ProSerGlyHisProGlnInProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCATCTGACATCTCTCAAGCCCGCTGCGCATACCCCTGCTGTGCAATCTCTGTCCT 186  
QY 41 GlyLeuIysGlyAspAlaGlyGlyIleGlyAspIleGlyAlaPProGlyArgProGlyArg 60  
DB 187 GGCTCAAGAGGAGATGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246  
QY 61 ValGlyProThrArgIleGlyIleGlyGlyAspMetCysIleAspIleGlyIleGlySerValGly 80

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DB 247 GTCCGCCCCCGGAGAGAAAAAGAGACATGGGGGCAAGACAGACAGATGTGGGT 306
QY 81 ArgHieGlyValIleGlyProIleGlySerIleGlyGlyValIleGlyAspSerGlyAspIle 100
DB 307 CGTCATGAGAAAAATGTGCTCCATGGCTCTAAAGGTGAGAAAGAGATTCCGGTGACATA 366
QY 101 GlycerolProGlyProAsnGlyGlyProGlyLeuProGlyProGlyGlySerGlyLeuArgIle 120
DB 367 GGACCCCTGGTCTTAATGAGAACACAGCCCTCCATGTGAGTGACGACCTCGCAAG 426
QY 121 AlaIleGlyGlyMetAspAsnGlyValSerGlyLeuThrSerGlyLeuValPheIleIys 140
DB 427 GCCATCGGGGAGATGAGACACAGGTCTCTCAGCTGACGACGACGACCTCAATTATCAAG 486
QY 141 AsnAlaValAlaGlyValArgGlyThrGlySerIleIleIleValLeuValIleGlyGly 160
DB 487 AATGCTGTGCGCGGTGTCGCGAGACGAGACGAGCAAGATCTACCTGCTGTGAGAGAGAG 546
QY 161 LysArgGlyValAlaAspAlaGlyLeuSerGlyGlyGlyValIleGlyValIleThrLeuSerMetPro 180
DB 547 AAGGCTTACGCGAGAGCCAGCTGTCTGCAAGGCGCGGAGGACGCTAGACATGCC 606
QY 181 LysAspGlyValAlaAsnGlyLeuMetAlaAlaIleValAlaGlyValIleValArg 200
DB 607 AAGGACGAGGCTGCGCAATGCGCTGATGCGCATACCTGCGGCAAGCGCGCTGCCCGT 666
QY 201 ValPheIleGlyIleAsnAspLeuGlyValGlyValIlePheValIleValIleSer 220
DB 667 GTCTTCATCGGACATCAAGACCTGAGAGAGAGGCGCTTCGTGTCTCTGACCACTCC 726
QY 221 ProMetArgThrPheAsnIleThrPheSerGlyGlyProAsnAlaAlaIleValAspGlyGly 240
DB 727 CCATGCGGACCTTCAACAGATGGCGGCGGCTGAGCCCAACATGCTTACGACGAGAG 786
QY 241 AspCysValGlyMetValAlaSerGlyGlyIleThrPheAspValAlaCysValIleThrMet 260
DB 787 GACTGCGGAGATGATGTGCTCGGCGGCTGAGAACGACGCTGCGCACCACCACTG 846
QY 261 TyrPheMetCysGlyPheAspGlyLeuMet 271
DB 847 TACTTCATGTGTGAGTTGACAGAGAACATG 879

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## RESULT 3

AACS8385  
ID AACS8385 standard; cDNA; 1238 BP.

AC AACS8385;

DT 29-JAN-2001 (first entry)

DE Human PRO1182 nucleotide sequence SEQ ID NO:50.

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
 KW neurotrophic; neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; angiogenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
 KW epithelial disorder; retinal disorder; blastocoele disorder;  
 KW inflammatory disorder; immunologic disorder; ss.

XX Homo sapiens.

OS WO200053755-A2.

PN 14-SEP-2000.

XX 06-JAN-2000; 2000WO-US000376.

XX 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

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PR 07-JUN-1999; 99US-0143048P.
PR 26-JUN-1999; 99US-0145688P.
PR 30-NOV-1999; 99WO-US028313.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (BETH ) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA,
PI Wetanabe CK, Wood WI,
XX
DR WPI: 2000-572270/53.
DR P-PSDB; AAB24075.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer.
XX
PS Claim 50; Fig 37; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to one of
CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, PRO619,
CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC and prevention of cancer. The antibodies and other anti-tumour compounds
CC maybe used to treat various conditions, including those characterised by
CC overexpression and/or activation of the amplified PRO genes. Exemplary
CC conditions or disorders to be treated with such antibodies and other
CC compounds include benign or malignant tumours (e.g., renal, liver,
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, and
CC glioblastomas), and various head and neck tumours), leukaemia and
CC lymphoid malignancies, other disorders such as neuronal, glial,
CC astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC seromal and blastocoele disorders, and inflammatory, angiogenic and
CC immunologic disorders. AACS8242 to AACS8366 represent PCR primers and
CC hybridisation probes used in the isolation of the human PRO sequences.
CC AACS8367 to AACS8386 and AAB24057 to AAB24089 represent human PRO
CC polynucleotide and protein sequences given in the exemplification of the
CC present invention
XX
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

```

## Alignment Scores:

Pred. No.: 9,91e-263 Length: 1238  
 Score: 271.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x AACS8385 (1-1238)

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QY 21 ProSerGlyValIleProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
DB 127 CCATCTGACATCTCTACGCGGCTGCGATGACGCTGCTGTGTGACATCTCTGTCCT 186
QY 41 GlyLeuValGlyValAspAlaGlyValIleGlyValIleGlyValIlePheProGlyValArg 60
DB 187 GGCTCTAAGAGGGGATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 61 ValGlyProThrGlyValIleGlyValIleGlyValIleGlyValIleGlyValIleGly 80
DB 247 GTGCGCCCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY 81 ArgHieGlyValIleGlyProIleGlySerIleGlyGlyValIleGlyValIleGlyValIle 100

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Db      367  GGACCCCTGGTCTTAATGAGAAACCAAGGCTCCCATGTGAGTGACGACGATGGGCAAG 426
Qy      121  A1a1leG1yG1uMeAaPaaNG1nValSerG1nLeuThrSerG1uLeuLeuPhe1le1yS 140
Db      427  GCCATCGGGAGAGATGACAAACCAAGGTCTCTCAGCTGACCAAGGACCTCAAGTTCATCAG 486
Qy      141  AaNa1aVal1a1aG1yValArG1uThrG1uSer1yS1e1y1yLeuLeuVal1yS1uG1u 160
Db      487  AATGCTGTGCGCGGTGTGCGGAGACGAGACCAAGATCTTACTCTCTGTAAGAGAGAG 546
Qy      161  LySaArG1y1yA1aAaP1aG1nLeuSerCySg1nG1yArG1yG1y1yThrLeuSerMePro 180
Db      547  AAGCGCTACGGCGGAGCGCCAGCTGTCTGCGCAGGGCCGCGGGGCGACCGCTGAGCATGCC 606
Qy      181  LySaAaP1u1a1a1aAaNG1yLeuMe1a1a1y1yLeuA1a1a1y1yLeuA1a1a1y 200
Db      607  AAGGACGAGGCTGCGCAATGCGCTGATGGCCGCTACCTGGCGCAAGCCGGCCTGGCCCGT 666
Qy      201  ValPhe1leG1y1yLeuAaAaP1eNG1u1ySg1uG1yA1aPheVal1y1ySerAaP1eS 220
Db      667  GTCTTCATCGCATCAACGACCTGAGAGAGAGGCGCCTTGTGTACTCTGACCACTCC 726
Qy      221  ProMe1a1y1yThrPheAa1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 240
Db      727  CCCATGCGGACCTTCAACAAAGTGCGCGAGCGGTGAGCCCAACATGCTTACGACGAGAG 786
Qy      241  AaP1ySg1yVal1yMe1yA1a1a1eSg1yG1y1y1y1y1y1y1y1y1y1y1y1y1y1y 260
Db      787  GACTGCGTGAATGATGTGCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 846
Qy      261  TyrPheMeCySg1yPheAaP1ySg1uAaP1eMet 271
Db      847  TACTTCATGTGTGACTTTGACAGAGAAACATG 879

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PR      20-DEC-1999; 99WO-US030911.
PR      05-JAN-2000; 2000WO-US000219.
PR      06-JAN-2000; 2000WO-US000376.
PR      11-FEB-2000; 2000WO-US000365.
PR      18-FEB-2000; 2000WO-US0004341.
PR      22-FEB-2000; 2000WO-US0004414.
PR      24-FEB-2000; 2000WO-US0004914.
PR      24-FEB-2000; 2000WO-US0005004.
PR      02-MAR-2000; 2000WO-US0005841.
PR      15-MAR-2000; 2000WO-US0006884.
PR      20-MAR-2000; 2000WO-US0007377.
XX
XX      (GENENTECH INC.
XX
XX      Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
XX      Ferrare N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
XX      Grimaldi CJ, Gurney AL, Klijavin IY, Napier MA, Pan J, Paoni NF,
XX      Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX      Zhang Z;
XX      WPI; 2001-032160/04.
XX      P-PSDB; AAB65261.
XX
XX      PRO polynucleotides used to produce polypeptides used to target bioactive
XX      molecules such as toxins, radiolabels or antibodies, to specific cells,
XX      to cause targeted cell death.
XX
XX      Claim 2; Fig 251; 935pp; English.
XX
XX      The present invention describes human secreted and transmembrane PRO
XX      proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX      be used for targeted delivery of bioactive molecules, such as toxins,
XX      radiolabels or antibodies, that cause cell death. PRO nucleotide
XX      sequences, and their fragments, can be used as hybridisation probes, in
XX      chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX      DNA. They may also be used to produce transgenic animals which are used
XX      to develop and screen therapeutically useful reagents. The PRO nucleotide
XX      and protein sequence can be used for tissue typing and in treating
XX      cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX      CC AAF44470 represent PCR primers and hybridisation probes used in the
XX      isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
XX      CC AAB65300 represent human PRO polynucleotide and protein sequences given
XX      in the exemplification of the present invention
XX
XX      Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
XX
XX      Alignment Scores:
XX      Pred. No.: 9,91e-263 Length: 1238
XX      Score: 271.00 Matches: 271
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 100.00% Indels: 0
XX      DB: 5 Gaps: 0
XX
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Qy      1  Me1a1yG1yAa1yMe1a1yA1a1e1yG1yVal1yLeu1e1ySer1e1yA1a1e1ySer1e1yLeu 20
Db      67  ATGAGGGGGAATCTGCGCCTGCTGTGAGGCGTCTTAATGACGCTGCGCTTCTCTCACTGCTG 126
Qy      21  ProSerG1yH1sProG1nProA1aG1yAaP1aP1aCySg1yA1aP1aG1yA1aP1aG1yA1a 40
Db      127  CCATCTGACATCTCTCAAGCCGCGCTGCGCATACCGCTGCTGTGCGAGATCTCTGCTCCT 186
Qy      41  G1yLeu1ySg1yAaP1a1aG1yG1y1ySg1yAaP1ySg1yA1aP1aG1yA1aP1aG1yA1a 60
Db      187  GGCCTCAAGAGGATCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
Qy      61  ValG1yProThrG1yG1y1ySg1yAaP1e1yAaP1ySg1yG1y1y1ySg1ySer1yA1y 80
Db      247  GTCGCGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
Qy      81  ArgH1sG1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 100

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Db      307  CGTCTGAGAAAATTGGTCCCTTAAAGGTGAGAAAGGATTCCGGTACCTA 366
Qy      101  GYProProGlyYProAsnGlyYgluProGlyLeuProGlyCysSerGlnLeuArglys 120
Db      367  GGAACCCCTGGTCTTAATGAGAACCAAGGCTCCCATGTGATGAGCAGCTGGCAG 426
Qy      121  AAlaIleGlyIleuMetAspAsnGlnIvalSerGlnLeuThrSerGlnLeuLysPheIleLys 140
Db      427  GCCATCGGGAGATGACCAACAGGCTCTCAAGCTGACGACGAGCAGCTCAATTCATCAAG 486
Qy      141  AsnAlaValAlaGlyValArgGluThrGluSerLysIleTyrLeuLeuValLysGluGlu 160
Db      487  AATGCTGTGCGCGGTGCTGCGCAGACGAGACGACCAAGATCTACTGCTGTAGAGAGAG 546
Qy      161  LysAlaGlyTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyTyrThrLeuSerMetPro 180
Db      547  AAGCCCTACGGCGGAGCCCAAGCTGTCTGCGCAGGCGCGGGGCGCAGCTGAGCATGCC 606
Qy      181  LysAspGluAlaAlaAsnGlyIleuMetAlaIleTyrLeuAlaGlnAlaGlyLeuAlaArg 200
Db      607  AAGGACGAGGCTGCGCAATGGCTGATGGCCGCAATCTGGCGCAGCCGCGCTGGCCGT 666
Qy      201  ValPheIleGlyIleAsnAspLeuGluIuYsgluGlyAlaPheValTyrSerAspHisSer 220
Db      667  GTCTTCATCGGCATCAACGACCTGAGAGAGAGGCGCGCTTCGTACTCTGACCATCTCC 726
Qy      221  ProMetAlaGlyThrPheAsnLysIleTyrArgSerGlyIlePheAsnAlaIleTyrAspGlu 240
Db      727  CCCAAGCGGACCTTCAACAGTGGCGCAGCGGTGAGCCCAACATGCTTACGACGAGAG 786
Qy      241  AspCysValIleGluMetValAlaSerGlyIleTyrPheAspValAlaCysHisThrThrMet 260
Db      787  GACTCCGCGAGATGCTGCTGCTGGGCGGCTGGAAACGCTGGCTGCACACCAACATG 846
Qy      261  TyrPheMetCysGluPheAspLysGluAsnMet 271
Db      847  TACTTCATGTGTGAGTTTGACAGAGAAACATG 879

RESULT 5
ABL88155
ID      ABL88155 standard, cDNA, 1238 BP.
XX      ABL88155;
XX      16-MAY-2002 (first entry)
DE      Human PRO1182 cDNA sequence SEQ ID NO:167.
XX      Human; angiogenesis; cardiact; cytostatic; antiangiogenic; hypotensive;
XX      gene therapy; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX      angiogenic disorder; cardiovascular disorder; endothelial disorder; cancer;
XX      age-related macular degeneration; arterial restenosis; angina;
XX      rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX      lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX      wound healing; chromosome mapping; gene mapping; gene; ss.
OS      Homo sapiens.
XX      WO200200690-A2.
XX      03-JAN-2002.
XX      20-JUN-2001, 2001WO-US019692.
XX      23-JUN-2000, 2000US-0213637P.
XX      20-JUL-2000, 2000US-0219556P.
XX      25-JUL-2000, 2000US-0220624P.
XX      25-JUL-2000, 2000US-0220664P.
XX      28-JUL-2000, 2000US-0220710.
XX      02-AUG-2000, 2000US-0222695P.
XX      17-AUG-2000, 2000US-00643657.

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PR      23-AUG-2000, 2000WO-US023522.
PR      24-AUG-2000, 2000WO-US023328.
PR      07-SEP-2000, 2000US-0230978P.
PR      18-SEP-2000, 2000US-00664610.
PR      18-SEP-2000, 2000US-00665350.
PR      24-OCT-2000, 2000US-0242922P.
PR      08-NOV-2000, 2000US-00709238.
PR      08-NOV-2000, 2000WO-US030952.
PR      10-NOV-2000, 2000WO-US030873.
PR      01-DEC-2000, 2000WO-US032678.
PR      20-DEC-2000, 2000US-00747259.
PR      20-DEC-2000, 2000WO-US034956.
PR      22-JAN-2001, 2001US-00767609.
PR      28-FEB-2001, 2001US-00796498.
PR      28-FEB-2001, 2001WO-US006520.
PR      01-MAR-2001, 2001WO-US006666.
PR      09-MAR-2001, 2001US-00802706.
PR      14-MAR-2001, 2001US-00808689.
PR      22-MAR-2001, 2001US-00815744.
PR      05-APR-2001, 2001US-00828366.
PR      10-MAY-2001, 2001US-00854208.
PR      10-MAY-2001, 2001US-00854280.
PR      25-MAY-2001, 2001US-00866028.
PR      25-MAY-2001, 2001US-00866034.
PR      25-MAY-2001, 2001US-00870992.
PR      30-MAY-2001, 2001US-00870574.
PR      30-MAY-2001, 2001WO-US017443.
PR      01-JUN-2001, 2001WO-US017800.
XX      (GETH ) GENENTECH INC.
XX      Baker KP, Ferrara N, Garber H, Gerritsen ME, Goddard A,
XX      Godowski PU, Gurney AL, Hallian KJ, Matsters SA, Pan J,
XX      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX      WPI; 2002-090516/12.
XX      P-PDB; ABB84900.
XX      DR      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX      PT      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX      PT      infarction), endothelial or angiogenic disorders in a mammal.
XX      PS      Claim 2; Fig 167; 565bp; English.
XX      CC      ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX      CC      ABB85003. The PRO proteins and polynucleotides have cardiact, cytostatic,
XX      CC      antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
XX      CC      activities, and can be used in gene therapy. The PRO polynucleotides,
XX      CC      proteins, agonists and antagonists are useful for treating or diagnosing
XX      CC      cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
XX      CC      cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
XX      CC      atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX      CC      angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX      CC      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX      CC      healing. The PRO polynucleotides have applications in molecular biology,
XX      CC      including use as hybridisation probes, and in chromosome and gene
XX      CC      mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX      CC      exemplification of the present invention.
XX      SQ      Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9, 91e-263
Score:          271.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:    100.00%
DB:             6
Gaps:           0

US-09-806-277A-6 (1-271) x ABL88155 (1-1238)
Qy      1 MetArgGlyAsnLeuAlaLeuValGlyValLeuIleSerLeuAlaPheLeuSerLeuLeu 20

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Db	67	ATGAGGGGGAAATCTGGCCCTGGTGGGGCGTTCTTAATGACGCTGGCCCTTCCGTGATCGTGTG	128
Qy	21	ProSerGIYHieProGInProAlaGIYAaPAPAlaCYseServalGInIleUValPro	40
Db	127	CCATCTGGACATCTCTCAGCGCGGTGGATGAAGCGCTGCTCTGTGAAGATCTCTGTCCTT	186
Qy	41	GIYleuLYaGIYAaPAlaGIYGIuLYaPAlaYAsPLeYGIYAlaProGIYAArgProGIYArg	60
Db	187	GGCCTTCAGGGGATGCGGGAGAGAAAGGAGACAAAGAGCCCCCGAGCGGCTTGGAGAG	246
Qy	61	ValGIYProThrGIYGIuLYaPAlaYAsPLeYGIYAlaProGIYAArgProGIYArg	80
Db	247	GTGGGCCCCACGGAGAGAAAGAGAGCATGTGGGGACAAAGACAGAAAGCAAGTGTGGGT	306
Qy	81	ArgHlaGIYLYaIleGIYProIleGIYSerLYaGIYGIuLYaPAlaYAsPLeYGIYAlaPro	100
Db	307	CGTCATAGGAAAAATTTGGTCCCATTTGGCTCTCAAAAGGTGAAGAAAGAAATTCGGGTGACATA	366
Qy	101	GIYProProGIYProaPnGIYGIuLYaPAlaYAsPLeYGIYAlaProGIYArgProGIYArg	120
Db	367	GGACCCCCCTGGTCTTAATGGAGAACAGGCTCCCATGTGAAGTGAAGCCAGCTCGGCAAG	426
Qy	121	AlaIleGIYGIuLYaPAlaYAsPLeYGIYAlaProGIYArgProGIYArg	140
Db	427	GGCATCGGGAGATGTGACAAACCGGTCTCTCACTGACCGACGAGCTCAAGTTCATCAAG	486
Qy	141	AsnAlaValAlaGIYValaArgGIYThrGIYSerLYaIleThrLeuValaLYaGIuLYa	160
Db	487	ATGTCTGTGCGCGGTGTGGCGAGACGAGACGAAAGTCTTACTCTGTGTGAAGAGAG	546
Qy	161	LYaArgTYAlaAsPAlaGInLeuSerCYaGIYArgIYThrLeuSerMetPro	180
Db	547	AAGCGCTAAGCGGAGCCCGACGCTGTCTCGACAGGCGCGGGGACAGCTGAACATAGCCC	606
Qy	181	LYaAsPAlaAlaAlaPnGIYLeuMetAlaAlaTYrLeuAlaGInIleGIYLeuAlaArg	200
Db	607	AAGAGAGAGCGTGGCCATAGGCTGATGGCCGCACTTGGCGAGCGGCGCTGGCCCGT	666
Qy	201	ValIleIleGIYIleAsnAPLeuGIYLYaGIYAlaIleValTYrSerAsPAlaSer	220
Db	667	GTCTTCATGGGATCAACGACCTGGAGAGAGAGGGCGCTTGGTGACTGTGACACTCC	726
Qy	221	ProMetArgThrPheAsnLYrTPdArgSerGIYGIuProAsnAlaTYrAsPAlaGIu	240
Db	727	CCCATGCGGACCTTCAACAAAGTGGCCAGCGGTGAAGCCCAATGCTCTCGACGAGAG	786
Qy	241	AsPAlaValaGIuMetValaIleSerGIYGIYTPAsnAsPAlaIaCYHstThrMet	260
Db	787	GACTGCTGAAGATGTGGCTTGGGCGGCTGGAGACGATGGCTGGCCACACACCATG	846
Qy	261	TYrPheMetCYaGIuPheAsPAlaYAsPLeYGIYAlaProGIYAArgProGIYArg	271
Db	847	TACTTCATGTGTGAGTTTGACAGAGAGAACATG	879
RESULT 6			
ID ABL95644 standard, cDNA, 1238 bp.			
AC	ABL95644;		
XX			
DT	19-JUL-2002 (first entry)		
DE	Human angio genesis related cDNA PRO1182 SEQ ID NO: 167.		
XX			
KW	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;		
KW	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;		
KW	cardiac; cytolethic; antiangiogenic; hypotensive; vulnerary;		
XX	antiarteriosclerotic; gene; ss.		
OS	Homo sapiens.		
XX			
PN	WO200208284-A2.		
XX			

PD	31-JAN-2002.
XX	
PF	09-JUL-2001; 2001WO-US021735.
XX	
PR	20-JUL-2000; 2000US-0219556P.
PR	25-JUL-2000; 2000US-0220624P.
PR	25-JUL-2000; 2000US-0220664P.
PR	28-JUL-2000; 2000WO-US020710.
PR	02-AUG-2000; 2000US-0222695P.
PR	17-AUG-2000; 2000US-00643657.
PR	23-AUG-2000; 2000WO-US023352.
PR	24-AUG-2000; 2000WO-US023328.
PR	07-SEP-2000; 2000US-0230978P.
PR	18-SEP-2000; 2000US-00664610.
PR	18-SEP-2000; 2000US-00665350.
PR	24-OCT-2000; 2000US-0242922P.
PR	08-NOV-2000; 2000US-00709238.
PR	08-NOV-2000; 2000WO-US030952.
PR	10-NOV-2000; 2000WO-US030873.
PR	01-DEC-2000; 2000WO-US032878.
PR	20-DEC-2000; 2000US-00747259.
PR	20-DEC-2000; 2000WO-US034556.
PR	22-JAN-2001; 2001US-00767609.
PR	28-FEB-2001; 2001US-00796498.
PR	28-FEB-2001; 2001WO-US006520.
PR	01-MAR-2001; 2001WO-US006666.
PR	09-MAR-2001; 2001US-00802706.
PR	14-MAR-2001; 2001US-00806689.
PR	22-MAR-2001; 2001US-00816744.
PR	05-APR-2001; 2001US-00828566.
PR	10-MAY-2001; 2001US-00854208.
PR	10-MAY-2001; 2001US-00854280.
PR	25-MAY-2001; 2001US-00866028.
PR	25-MAY-2001; 2001US-00866034.
PR	30-MAY-2001; 2001US-00870574.
PR	30-MAY-2001; 2001WO-US017443.
PR	01-JUN-2001; 2001WO-US017800.
XX	20-JUN-2001; 2001WO-US019692.
XX	
PA	(GETH ) GENENTECH INC.
PA	(BAKE ) BAKER K P.
PA	(FERR ) FERRARA N.
PA	(GERB ) GERBER H.
PA	(GERR ) GERRITSEN M E.
PA	(GODD ) GODDARD A.
PA	(GODO ) GODOWSKI P J.
PA	(GURN ) GURNEY A L.
PA	(HILL ) HILLMAN K J.
PA	(HILL ) HILLMAN K J.
PA	(MARS ) MARSTERS S A.
PA	(PANT ) PAN J.
PA	(PAON ) PAONI N F.
PA	(STEP ) STEPHAN J F.
PA	(WATA ) WATANABE C K.
PA	(WILL ) WILLIAMS P M.
PA	(WOOD ) WOOD W I.
XX	
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI	Godowski PJ, Gurney AL, Hillman KJ, Marsters SA, Pan J,
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX	
DR	WPI, 2002-171999/22.
XX	
DR	P-PSDB; ABB95506.
XX	
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal.
XX	
PS	Claim 1; Fig 167; 567pp; English.
XX	
CC	The present invention provides the protein and coding sequences of human
CC	PRO proteins. These are useful for treating or diagnosing a
CC	cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial resection, rheumatoid arthritis,  
CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention  
XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	9,91e-263	Length:	1238
Score:	271.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-806-277a-6 (1-271) x ABL95644 (1-1238)

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Db 67 ATGAGGGGGAATCTGGCCCTGGTGGCGCTTCTAATCAGCCCTGGCTTCTCTCATCTGCTG 126
QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40
Db 127 CCATCTGGACATCTCTCAGCCGCGCTGGCGCATGACGCTGCTCTGTGACAGATCTCTGCTCC 186
QY 41 GlyLeuLysGlyAspAlaGlyGluLysGlyAspLysGlyValProGlyValArgProGlyVal 60
Db 187 GGCTTCAGAGGAGATCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 61 ValGlyProThrGlyGlyLysGlyAspMetGlyAspLysGlyGlnLysGlySerValGly 80
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DT 17-JUN-2003 (first entry)
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KW Virus; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PBO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; Leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.
XX
OS Homo sapiens.
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XX
PD 02-JAN-2003.
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PF 19-NOV-2001; 2001US-00899734.
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XX  
XX (GERTH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gottlieb ME, Goddard A,  
PI Grimaldi JC, Gurney AL, Kijavlin IV, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT,  
PI Zhang Z;  
XX  
DR WPI; 2003-352829/33.  
DR P-PSDB; AB072552.  
XX  
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
PT disease.  
XX  
PS Claim 1; Fig 251; 663pp; English.  
XX  
XX The invention describes a new isolated nucleic acid molecule comprising  
CC the full length coding sequence of the DNA deposited with the American  
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PFA, 819-PFA,  
CC 209439, 203135, etc.) or a sequence with at least 80% identity to a DNA  
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
CC are particularly useful for detecting or treating e.g. malignancies or  
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,

CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
CC disease in mammals. The PRO polypeptides are useful in drug screening,  
CC particularly as targets for therapeutic intervention in these diseases,  
CC and in the diagnostic determination of the presence of these diseases.  
CC The PRO polypeptides are also useful as molecular weight markers, or for  
CC chromosome identification. The PRO genes are useful as hybridisation  
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
CC The PRO genes may also be used in gene therapy, particularly for  
CC replacing a defective gene. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide  
XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: Length: 1238  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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QY 21 ProSerGlyHisProGlnProAlaGlyAspAspAlaCysSerValGlnIleLeuValPro 40  
DB 127 CCATCTGACATCCTCAAGCGCGGCTGGGATACCGCTGCTGTGGCAGATCCTGCTCCT 186  
QY 41 GlyLeuLysGlyAspAlaGlyValGlyLysGlyAspLysGlyAlaProGlyValProGlyValArg 60  
DB 187 GGCCTCAAGGGGATGCGGAG 246  
QY 61 ValGlyProThrGlyValGlyValGlyValAspMetGlyAspLysGlyValGlyValGlyValGly 80  
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DB 367 GGACCCCTGCTCTTAATGAG 426  
QY 121 AlaIleGlyIleMetLeuAspAsnGlnValSerGlnIleuThrSerGlyLeuValPheIleLys 140  
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DB 487 AATGCTGTGCGCGGTGTGCGGAG 546  
QY 161 LysAlaGlyTyrAlaAspAlaGlnLeuSerCysGlnGlyArgGlyValGlyValThrLeuSerMetPro 180  
DB 547 AAGGCTAAGCGGAG 606  
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Db 847 TACTTCATGTGTGAGTTTGACAGAGAACTG 879

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DT 22-APR-2003 (first entry)  
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XX  
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;  
KW tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodng therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US203027162-A1.  
XX  
PD 06-FEB-2003.  
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PE 15-NOV-2001; 2001US-00997428.  
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XX 28-AUG-2001; 2001US-0089951P.
XX (GENTH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers J, Eaton DL,
XX Ferrara N, Fong S, Gerber H, Gerlicsen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Gurney AL, Kijavrin IJ, Napier MA, Pan J, Paoni NF,
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z,
XX WPI; 2003-340824/32.
XX P-PSDB; ABC25998.
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX and are therapeutically useful for enhancing immune responses.
XX Claim 2; Fig 251; 661pp; English.
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for linking
XX bioactive molecules to cells expressing PRO polypeptides, for modulating
XX biological activities of cells expressing PRO polypeptides, and for for
XX identifying agonists or antagonists. The polynucleotide sequences
XX encoding PRO polypeptides are useful as hybridisation probes, in
XX chromosome and gene mapping, in the generation of antisense RNA and DNA,
XX in the preparation of PRO polypeptides, for generating transgenic animals
XX or knockout animals, to construct hybridisation probes for mapping the
XX gene which encodes the PRO polypeptide, and for the genetic analysis of
XX individuals with genetic disorders, in gene therapy, for chromosome
XX identification, as chromosome markers, and for generating probes for PCR,
XX Northern analysis, Southern analysis and Western analysis. The present
XX sequence encodes a human PRO polypeptide of the invention. Note: The
XX sequence data for this patent was obtained in electronic format directly
XX from the USPTO web site at seqdata.uspto.gov/patseqidentry.html
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 9,91e-263 Length: 1238
XX Score: 271.00 Matches: 271
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 8 Gaps: 0
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XX US-09-806-277A-6 (1-271) x ACD44367 (1-1238)

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Db 187 GGCCTCAAGAGGGATGGCGGAGAGAGAGAGCAAAAGCGCCCGGAGCGGCTGGAGAGA 246  
QY 61 ValGlyProThrGlyGlyIleYsgIyAspMetGlyAspYsgIyGlyIleYsgIySerValGly 80  
Db 247 GTCCGCCCCACGGAGGAGAGAGAGACATGGCGGAGCAAGAGACAGAGCACTGGTGGT 306  
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QY 121 AlaIleGlyIleMetAspAsnGlnValSerGlnLeuThrSerGlnLeuLeuYpHeIleYs 140  
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QY 161 LysArgTyrAlaAspAlaGlnLeuSerCysGlnGlyYArgGlyYThrLeuSerMetPro 180  
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QY 201 ValPheIleGlyIleAsnAspLeuGlyIleYsgIyGlyIlePheValTyrSerAspHisSer 220  
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PN US2002142961-A1.  
XX 03-OCT-2002.  
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PR 15-SEP-1999; 99WO-US021547.  
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PR 01-DEC-1999; 99WO-US028634.  
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PR 18-FEB-2000; 2000WO-US004341.  
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 PR 24-FEB-2000; 2000WO-US005004.  
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 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
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 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX  
 PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Garber H, Gertlesen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-155950/15.  
 DR P-PSDB; ABUS9007.  
 XX

PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
 XX  
 PS Claim 2; Fig 251; 647pp; English.

CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 9,91e-263 Length: 1238  
 Score: 271.00 Matches: 271  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00%

DB: 8 Gaps: 0  
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 DT 16-JUL-2003 (first entry)  
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 DE Novel human secreted and transmembrane protein PRO1182 cDNA.  
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 KW Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185;  
 PRO943; PRO1133; PRO311; PRO363; PRO5723; PRO1114; PRO3101;  
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KM radiolabel; antibody; cell death; tissue typing; gene therapy;  
KM cytostatic; chromosome mapping; gene mapping; transgenic animal;  
KM knockout animal; immunohistochemical staining; gene; ss.  
XX Hemo sapiens.  
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PF 14-NOV-2001; 2001US-00993667.  
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## Alignment Scores:

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 Db 247 GTGCGCCCGCCGAG 306  
 QY 81 ArgHisGlyValIleGlyProIleGlySerLeuGlyGlyLeuGlyAspSerGlyAspIle 100  
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 QY 181 LysAspGlnAlaAlaAsnGlyLeuMetAlaAlaTyrLeuAlaGlnAlaGlyLeuAlaArg 200  
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 DT 22-APR-2003 (first entry)  
 XX XX  
 DE Novel human secreted or transmembrane protein PRO1155 DNA.  
 XX XX  
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; hemiplegia; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN US2003027985-A1.  
 XX XX  
 PD 06-FEB-2003.  
 XX XX  
 PF 14-NOV-2001; 2001US-00990562.  
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PR 02-JUN-1999; 99WO-US012252.  
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PR 20-JUL-1999; 99US-0147458P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
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PR 23-JUN-2000; 2000US-0213637P.  
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PR 11-AUG-2000; 2000WO-US022031.  
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Alignment Scores: 9.91e-263  
Pred. No.:  
Length: 1238





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XX Human; secreted and transmembrane protein; gene therapy; PRO; PRO943;  
KW PRO183; PRO184; PRO185; PRO131; PRO1133; PRO363; PRO5723; PRO1387;  
KW PRO114; PRO3301; PRO940; PRO1181; PRO1170; PRO361; PRO846;  
KW bioactive molecule; toxin; radiolabel; antibody; cell death; cancer;  
KW autoimmune disease; chromosome mapping; gene mapping; transgenic animal;  
KW knockout animal; septic shock; gene; ss.  
XX  
OS Homo sapiens.  
XX US2002177164-A1.  
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PD 28-NOV-2002.  
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PE 20-NOV-2001; 2001US-00869293.  
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XX 16-JUN-1997; 97US-0049787P.  
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PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089533P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089586P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021065.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
  
XX (GETH ) GENENTECH INC.  
PA  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Bertara N, Fong S, Gerner H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi UC, Garney AL, Kijavini JV, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2003-328481/31.  
DR P-PSDB; AB081674.  
XX  
XX  
PT New secreted and transmembrane polypeptide, useful for modulating  
PT biological activity of cell expressing the polypeptide, for identifying  
PT agonists or antagonists of polypeptide, and as molecular weight markers.  
PS Claim 2; Fig 251; 654pp; English.  
XX  
XX The invention describes an isolated, secreted and transmembrane  
CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting  
CC PRO943, PRO183, PRO184, PRO185, PRO331, PRO1133, PRO363, PRO5723,  
CC PRO1387, PRO114, PRO3301, PRO940, PRO1181, PRO1170, PRO361 or PRO846  
CC polypeptide comprising contacting the sample with the polypeptide and  
CC determining formation of a polypeptide conjugate. (I) is also useful for  
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a  
CC cell expressing the above polypeptides to cause cell death. (I) is also  
CC useful as a therapeutic agent e.g. for treating cancer and autoimmune  
CC disease. PRO is useful in assays to identify other proteins or molecules  
CC involved in binding interactions. The polynucleotide (II) encoding (I) is  
CC useful in chromosome and gene mapping, for generating transgenic animals  
CC or knockout animals which in turn are useful in the development and  
CC screening of therapeutically useful reagents, for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome

CC Identification, and as a chromosome marker. An anti-(I)-antibody is  
CC useful in diagnostic assays for PRO, e.g. detecting its expression in  
CC specific cells, tissues or serum, for affinity purification of PRO, and  
CC for treating septic shock. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide  
XX

SO Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

## Alignment Scores:

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Best Local Similarity:	100.00%	Mismatches:	0
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US-09-806-277A-6 (1-271) x ACA67996 (1-1238)

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QY     101 GlyProProGlyProAenGlyGlyIuProGlyLeuProCySGIuCySeraGlyInLeuAArgLYs 120
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Db     367 GGACCCCTGGTCCTAATGAGAACCAAGGCTCCCATGTGATGACGACCACTGGCGAAG 426
QY     121 AAlIleGlyIuMetAAspAenGlyValSerGInLeuThrSerGlyLeuLYSPhelIeLYs 140
      |||
Db     427 GCCATCGGGAGATGACCAACCAAGGCTCTCTCAGCTGACCAAGAGCTCAAGTTCATCAAG 486
QY     141 AenAAlaValAAlaGlyValAArgIuThrGlySerLYSILETYrLeuLeuValLYSGIuGly 160
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QY     161 LYsAArgTYrAlaAspAAlaGInLeuSerCySGInGlyAArgGlyTYrThrLeuSerMetPro 180
      |||
Db     547 AAGCGCTACGCGGAGCGCCACGCTGCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCC 606
QY     181 LYsAAspGlyAAlaAAsenGlyLeuMetAAlaIATrLeuAAlaGInIleGlyLeuAAlaArg 200
      |||
Db     607 AAGGACGAGGCTGCAATGCGCTGATGGCCGATACCTGGCGCAAGCGGCTGGCCCGT 666
QY     201 ValPheIleGlyIleAAspAAspLeuGlyIuLYSGIuGlyAAlaPheValTYrSerAAspHisSer 220
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Db     667 GTCTTTCATCGGCACTCAAGCACTTGAAGAAAGAGGGCGCTTCTGTACTGTGACCACTCC 726
QY     221 ProMetAArgThrPheAenLYSTrAArgSerGlyGlyIuProAAspAAlaIATrAAspGlyIu 240
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Db     727 CCCATGCGGACCTTCAACCAAGTGGCGCAGCGGTGAGCCCAATGCTTACGACGAGGAG 786
QY     241 AAspCySeraValGlyMetValAAlaSerGlyGlyIuTrpAAspValAAlaCySeriThrThrMet 260
      |||
Db     787 GACTGCGTGAAGATGTGGCCCTCGGGCGGCTGGAACGAGGTGGCTGCACACCAACCATG 846
QY     261 TyrPheMetCySGIuPheAspLYSGIuAAsnMet 271
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Db     847 TACTTTCATGTGTGAGTTTGAACAAGGAAACATG 879
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

## SUMMARIES

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2	19	1.5	531	US-08-340-539A-5	Sequence 5, Appli
3	19	1.5	531	US-08-461-592B-5	Sequence 5, Appli
4	19	1.5	1829	5514582-1	Patent No. 5514582
5	19	1.5	2259	US-08-513-278-1	Sequence 1, Appli
6	19	1.5	2330	US-08-481-803-1	Sequence 1, Appli
7	19	1.5	2330	US-08-215-366A-1	Sequence 1, Appli
8	19	1.5	2330	US-08-340-539A-1	Sequence 1, Appli
9	19	1.5	2330	US-08-461-592B-1	Sequence 1, Appli
10	19	1.5	2354	US-09-023-655-1154	Sequence 1154, Ap
11	19	1.5	7244	US-08-378-313-26	Sequence 26, Appli
12	18	1.4	84	US-09-621-976-17318	Sequence 17318, A
13	18	1.4	89	US-09-401-064-288	Sequence 7799, Ap
14	18	1.4	290	US-09-401-064-288	Sequence 288, App
15	18	1.4	601	US-09-788-654A-17	Sequence 17, Appli
16	18	1.4	732	US-09-248-796A-13074	Sequence 13074, A
17	18	1.4	1361	US-09-016-434-1284	Sequence 1284, Ap
18	18	1.4	1366	US-09-200-965-1	Sequence 1, Appli
19	18	1.4	1506	US-09-252-991A-1159	Sequence 1159, Ap
20	18	1.4	2413	US-09-518-046-1	Sequence 1, Appli
21	18	1.4	2416	US-09-261-416-1	Sequence 1, Appli
22	18	1.4	2491	US-09-621-816B-1	Sequence 1, Appli
23	18	1.4	2544	US-09-518-046-3	Sequence 1, Appli
24	18	1.4	2667	US-09-252-991A-1396	Sequence 1396, Ap
25	18	1.4	2985	US-09-252-991A-1210	Sequence 1210, Ap
26	18	1.4	12118	US-09-788-654A-3	Sequence 3, Appli
27	18	1.4	38059	US-09-328-925-4	Sequence 4, Appli

28	18	1.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
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30	17	1.4	25	1	US-08-110-158-7	Sequence 7, Appli
31	17	1.4	178	4	US-09-513-999C-13111	Sequence 13111, A
32	17	1.4	291	4	US-09-313-294A-7401	Sequence 7401, Ap
33	17	1.4	426	4	US-09-252-991A-2270	Sequence 2270, Ap
34	17	1.4	426	4	US-09-513-999C-1213	Sequence 1213, Ap
35	17	1.4	443	4	US-09-621-976-9356	Sequence 9356, Ap
36	17	1.4	546	4	US-09-252-991A-2485	Sequence 2485, Ap
37	17	1.4	569	3	US-09-276-531-69	Sequence 69, Appli
38	17	1.4	614	4	US-09-513-999C-11545	Sequence 11545, A
39	17	1.4	705	4	US-09-252-991A-988	Sequence 988, App
40	17	1.4	756	1	US-08-681-812-3	Sequence 3, Appli
41	17	1.4	843	3	US-08-888-429A-25	Sequence 25, Appli
42	17	1.4	843	4	US-09-593-653-25	Sequence 25, Appli
43	17	1.4	906	4	US-09-206-166-4	Sequence 4, Appli
44	17	1.4	948	4	US-09-252-991A-2569	Sequence 2569, Ap
45	17	1.4	989	4	US-09-671-317-283	Sequence 283, App

## ALIGNMENTS

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RESULT 1
US-09-513-999C-36334
Sequence 36334, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 36334
LENGTH: 89
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 53
OTHER INFORMATION: v-a or c or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 54
OTHER INFORMATION: v-a or c or g
US-09-513-999C-36334

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-14; Length 89;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 43 GTTGGCTTACGCGCTGTCTCAGAGTGTGTCTCTGCTGCGCTCAGAGATG 92
Db 1 GTTGGCTTACGCGCTGTCTCAGAGTGTGTCTCTGCTGCGCTCAGAGATG 50

RESULT 2
US-08-340-539A-5
Sequence 5, Application US/08340539A
Patent No. 5808025
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 28
```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: FISH & NEAVE  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10020  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/340.539A  
;; FILING DATE: 16-NOV-1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/008,459  
;; FILING DATE: 25-JAN-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Gunnison, Jane  
;; REGISTRATION NUMBER: 38,479  
;; REFERENCE/DOCKET NUMBER: CG-104 CON  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-596-9000  
;; TELEFAX: 212-596-9030  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 531 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-08-340-539A-5

Query Match 1.5%; Score 19; DB 1; Length 531;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGACTGCGTGAGAT 823  
DB 361 AGGAGACTGCGTGAGAT 379

RESULT 3  
US-08-461-592B-5  
; Sequence 5, Application US/08461592B  
; Patent No. 5834425  
; GENERAL INFORMATION:  
; APPLICANT: Tedder, Thomas F.  
; APPLICANT: Kansas, Geoffrey S.  
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes  
; STREET: Ten Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,592B  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/340,539  
; FILING DATE: 16-NOV-1994

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/008,459  
;; FILING DATE: 25-JAN-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: CG-104  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 596-9000  
;; TELEFAX: (212) 596-9090  
;; TELEX: 14-8367  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 531 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-461-592B-5

Query Match 1.5%; Score 19; DB 2; Length 531;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGACTGCGTGAGAT 823  
DB 361 AGGAGACTGCGTGAGAT 379

RESULT 4  
5514582-1  
; Patent No. 5514582  
; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.  
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID  
; IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 43  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/185,670  
; FILING DATE: 21-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 986,931  
; FILING DATE: 08-DEC-1992  
; APPLICATION NUMBER: 808,122  
; FILING DATE: 16-DEC-1991  
; APPLICATION NUMBER: 440,625  
; FILING DATE: 22-NOV-1989  
; APPLICATION NUMBER: 315,015  
; FILING DATE: 23-FEB-1989  
; SEQ ID NO: 1:  
; LENGTH: 1829  
; 5514582-1

Query Match 1.5%; Score 19; DB 6; Length 1829;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGACTGCGTGAGAT 823  
DB 502 AGGAGACTGCGTGAGAT 520

RESULT 5  
US-08-513-278-1  
; Sequence 1, Application US/08513278  
; Patent No. 5840844  
; GENERAL INFORMATION:  
; APPLICANT: LASKY, LAURENCE A.  
; APPLICANT: STACHEL, SCOTT E.  
; APPLICANT: ROSEN, STEVEN D.  
; APPLICANT: SINGER, MARK S.  
; APPLICANT: YEDNOCK, TED A.



TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513.278  
FILING DATE: 10-AUG-1995  
CLASSIFICATION: 5530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/059027  
FILING DATE: 06-MAY-1993  
APPLICATION NUMBER: 07/786149  
FILING DATE: 31-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/315015  
FILING DATE: 23-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregler, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: 565D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2259 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-513-278-1  
Query Match 1.5%; Score 19; DB 2; Length 2259;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 805 AGGAGACTGCGTGGAGAT 823  
Db 502 AGGAGACTGCGTGGAGAT 520  
RESULT 6  
US-08-481-803-1  
Sequence 1, Application US/08481803  
Patent No. 5679346  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F. and Olivier G. Spertini  
TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481.803  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215.366  
FILING DATE: 21-MAR-1994  
APPLICATION NUMBER: US 07/720.602  
FILING DATE: 25-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/313.109  
FILING DATE: 21-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: CG-101 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1210  
US-08-481-803-1

Query Match 1.5%; Score 19; DB 1; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 805 AGGAGACTGCGTGGAGAT 823  
Db 465 AGGAGACTGCGTGGAGAT 483

RESULT 7  
US-08-215-366A-1  
Sequence 1, Application US/08215366A  
Patent No. 5776775  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F. and Olivier G. Spertini  
TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WHITE & CASE  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/215.366A  
FILING DATE: 21-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/720.602  
FILING DATE: 25-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/313.109  
FILING DATE: 21-FEB-1989

ATTORNEY/AGENT INFORMATION:  
NAME: Nels T. Lippert  
REGISTRATION NUMBER: 25,888  
REFERENCE/DOCKET NUMBER: 110604-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8582  
TELEFAX: (212) 354-8113  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1210  
US-08-215-366A-1

Query Match 1.5%; Score 19; DB 1; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 805 AGGAGACTGCGTGGAGAT 823  
DB 465 AGGAGACTGCGTGGAGAT 483

RESULT 8  
US-08-340-539A-1  
Sequence 1, Application US/08340539A  
Patent No. 5808025  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,539A  
FILING DATE: 16-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,459  
FILING DATE: 25-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Guntison, Jane  
REGISTRATION NUMBER: 38,479  
REFERENCE/DOCKET NUMBER: CG-104 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1207  
US-08-340-539A-1

Query Match 1.5%; Score 19; DB 1; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 805 AGGAGACTGCGTGGAGAT 823  
DB 465 AGGAGACTGCGTGGAGAT 483

RESULT 9  
US-08-461-592B-1  
Sequence 1, Application US/08461592B  
Patent No. 5834425  
GENERAL INFORMATION:

APPLICANT: Tedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Weingarten, Schurjin, Gagnebin & Hayes  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,592B  
FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/340,539  
FILING DATE: 16-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,459  
FILING DATE: 25-JAN-1993  
ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: CG-104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:

NAME/KEY: CDS  
LOCATION: 53..1210  
US-08-461-592B-1

Query Match 1.5%; Score 19; DB 2; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGACTGCTGGAGAT 823  
|||||  
DB 465 AGGAGACTGCTGGAGAT 483

## RESULT 10

US-09-023-655-1154  
; Sequence 1154, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocke, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC COMPATIBLE  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1154:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2354 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9187182  
US-09-023-655-1154  
Query Match 1.5%; Score 19; DB 4; Length 2354;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 AGGAGACTGCTGGAGAT 823  
|||||  
DB 465 AGGAGACTGCTGGAGAT 507

RESULT 11  
US-08-378-313-26/c  
; Sequence 26, Application US/08378313  
; Patent No. 6207881  
; GENERAL INFORMATION:  
; APPLICANT: THEOLOGIS, ATHANASIOS  
; APPLICANT: SATO, TAKAHIDO  
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
; NUMBER OF SEQUENCES: 34

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1018

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC COMPATIBLE  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/378,313  
;; FILING DATE:  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/862,493  
;; FILING DATE: 02-APR-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MORASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 29190-20002.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 856-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 706141  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7244 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: join(3056..3226, 3325..3453, 3539..3700, 4582  
;; LOCATION: ..5574)  
US-08-378-313-26

Query Match 1.5%; Score 19; DB 3; Length 7244;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1235 TTAAGTCCAAAAA 1253  
|||||

DB 645 TTAAGTCCAAAAA 627

## RESULT 12

US-09-621-976-17318  
; Sequence 17318, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17318  
; LENGTH: 84  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-17318

Query Match 1.4%; Score 18; DB 4; Length 84;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1236 TTAAGTCCAAAAA 1253

Db 62 TAAGTCCAAAAA 79

RESULT 13

US-09-621-976-7799  
; Sequence 7799, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO: 7799  
; LENGTH: 89  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-7799

Query Match 1.4%; Score 18; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 TAAGTCCAAAAA 1253  
Db 63 TAAGTCCAAAAA 80

RESULT 14

US-09-401-064-288/C  
; Sequence 288, Application US/09401064  
; Patent No. 6623923  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jianshun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Weagner, Madeline Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tonglong  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.471C2  
; CURRENT APPLICATION NUMBER: US/09/401,064  
; CURRENT FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 371  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 288  
; LENGTH: 290  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-401-064-288

Query Match 1.4%; Score 18; DB 4; Length 290;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 883 AGTTTGACAGAGACA 900  
Db 35 AGTTTGACAGAGACA 18

RESULT 15  
US-09-788-654A-17  
; Sequence 17, Application US/09788654A  
; Patent No. 673392  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al.

; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CU001143  
; CURRENT APPLICATION NUMBER: US/09/788,654A  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 17  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-788-654A-17

Query Match 1.4%; Score 18; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 AGTAGTCAGTAGTTAG 1239  
Db 163 AGTAGTCAGTAGTTAG 180

Search completed: December 17, 2004, 03:40:29  
Job time: 157 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2004, 11:23:35 ; Search time 103 Seconds

(without alignments)  
1870.134 Million cell updates/sec

Title: US-09-806-277A-6

Sequence: 1 MRGNALVGLISLAFSL.....NDVACHTMYMCEPKENM 271

## Scoring table:

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Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 824507 seqs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1643622

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO.spool.p/US09806277/runcat.15122004.101701.29786/app.query.fasta\_1.455  
-DB=Issued\_Patents\_NA -QFMT=fasta -SUPFIX=Oligo.rnt -MINMATCH=0.1 -LOOPT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09806277 @CGN 1.1.128 @runcat.15122004.101701.29786 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
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3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	4.1	89	4	US-09-513-999C-36334
2	10	3.7	93	2	US-08-481-658B-32
3	10	3.7	93	2	US-08-477-504A-32
4	10	3.7	93	2	US-08-486-756A-32
5	10	3.7	93	2	US-08-485-862B-32
6	10	3.7	93	3	US-08-787-739-32
7	10	3.7	93	3	US-08-487-077A-32
8	10	3.7	93	3	US-08-485-863A-32
9	10	3.7	93	3	US-08-178-115-32
10	10	3.7	93	3	US-09-177-776-32
11	10	3.7	93	3	US-09-772-719B-32
12	10	3.7	93	4	US-09-513-999C-36334

13	10	3.7	1397	1	US-07-964-589-1	Sequence 1, Appl
14	10	3.7	1397	5	PCT-US93-02024-1	Sequence 1, Appl
15	10	3.7	1399	4	US-08-335-469-1	Sequence 1, Appl
16	10	3.7	1399	4	US-08-260-190-1	Sequence 1, Appl
17	10	3.7	1401	2	US-08-481-658B-49	Sequence 49, Appl
18	10	3.7	1401	2	US-08-477-504A-49	Sequence 49, Appl
19	10	3.7	1401	2	US-08-486-756A-49	Sequence 49, Appl
20	10	3.7	1401	2	US-08-485-862B-49	Sequence 49, Appl
21	10	3.7	1401	3	US-08-787-739-49	Sequence 49, Appl
22	10	3.7	1401	3	US-08-487-077A-49	Sequence 49, Appl
23	10	3.7	1401	3	US-08-485-863A-49	Sequence 49, Appl
24	10	3.7	1401	3	US-08-485-049D-49	Sequence 49, Appl
25	10	3.7	1401	3	US-09-178-115-49	Sequence 49, Appl
26	10	3.7	1401	3	US-09-177-776-49	Sequence 49, Appl
27	10	3.7	1401	3	US-09-772-719B-49	Sequence 49, Appl
28	10	3.7	1522	2	US-08-481-658B-1	Sequence 1, Appl
29	10	3.7	1522	2	US-08-477-504A-1	Sequence 1, Appl
30	10	3.7	1522	2	US-08-486-756A-1	Sequence 1, Appl
31	10	3.7	1522	2	US-08-485-862B-1	Sequence 1, Appl
32	10	3.7	1522	3	US-08-787-739-1	Sequence 1, Appl
33	10	3.7	1522	3	US-08-487-077A-1	Sequence 1, Appl
34	10	3.7	1522	3	US-08-485-863A-1	Sequence 1, Appl
35	10	3.7	1522	3	US-08-485-049D-1	Sequence 1, Appl
36	10	3.7	1522	3	US-09-178-115-1	Sequence 1, Appl
37	10	3.7	1522	3	US-09-177-776-1	Sequence 1, Appl
38	10	3.7	1522	4	US-09-772-719B-1	Sequence 1, Appl
39	10	3.7	1522	4	US-08-260-190-5	Sequence 5, Appl
40	10	3.7	1522	4	US-08-260-190-23	Sequence 23, Appl
41	10	3.7	10898	2	US-08-481-658B-5	Sequence 5, Appl
42	10	3.7	10898	2	US-08-477-504A-5	Sequence 5, Appl
43	10	3.7	10898	2	US-08-486-756A-5	Sequence 5, Appl
44	10	3.7	10898	2	US-08-485-862B-5	Sequence 5, Appl
45	10	3.7	10898	3	US-08-787-739-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-09-513-999C-36334  
Sequence 36334, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Mline Edwards, J.B.  
APPLICANT: Duclerc, A.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 36334  
LENGTH: 89  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 53  
OTHER INFORMATION: v=a or c or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 54  
OTHER INFORMATION: v=a or c or g  
US-09-513-999C-36334  
Alignment Scores:  
Pred. No.: 0.0079  
Score: 11.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Length: 89  
Matches: 11  
Conservative: 0  
Mismatches: 0

Query Match: 4.06% Indels: 0  
DB: 4 Gaps: 0

US-09-806-277A-6 (1-271) x US-09-513-999C-36334 (1-89)

QY 3 GYAenLauAlaLeuValGlyValLeuIleSer 13  
DB 55 GGGATCTGGCCCTGTGGGCTTCTATACAC 87

## RESULT 2

US-08-481-658B-32

Sequence 32, Application US/08481658B  
Patent No. 5955075

## GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA

ZIP: 94920  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,658B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3E

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-435-2034

TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 93 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: 5th MN exon

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-481-658B-32

## Alignment Scores:

Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-481-658B-32 (1-93)

QY 53 GYAAlaProGlyArgProGlyArgValGly 62  
DB 51 GGGGCGCCCGGAGGAGCTGTGGCTGTGGC 80

## RESULT 3

US-08-477-504A-32

Sequence 32, Application US/08477504A  
Patent No. 5972353

## GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA

ZIP: 94920  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,504A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-435-2034

TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 93 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: 5th MN exon

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-477-504A-32

## Alignment Scores:

Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
Gaps: 0

US-09-806-277A-6 (1-271) x US-08-477-504A-32 (1-93)

QY 53 GYAAlaProGlyArgProGlyArgValGly 62  
DB 51 GGGGCGCCCGGAGGAGCTGTGGCTGTGGC 80

## RESULT 4

US-08-486-756A-32

Sequence 32, Application US/08486756A  
Patent No. 5981711

## GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court

CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,756A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-486-756A-32

Alignment Scores:  
Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-486-756A-32 (1-93)

QY 53 G1YAlAPrOg1YArPrOg1YArGvAlG1Y 62  
DB 51 GGGGGCCCCGGGAGGCGCTGGCGCTGTGGC 80

RESULT 5  
US-08-485-862B-32  
Sequence 32, Application US/08485862B  
Patent No. 5389838  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,862B

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/477,504  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-485-862B-32

Alignment Scores:  
Pred. No.: 0.0842 Length: 93  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 2 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-485-862B-32 (1-93)

QY 53 G1YAlAPrOg1YArPrOg1YArGvAlG1Y 62  
DB 51 GGGGGCCCCGGGAGGCGCTGGCGCTGTGGC 80

RESULT 6  
US-08-787-739-32  
Sequence 32, Application US/08787739  
Patent No. 6027887  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 369 Pine Street, Suite 610  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/787,739  
FILING DATE: 24-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,049  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,756  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/477,504

FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,658  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,862  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,863  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,077  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-787-739-32

Alignment Scores:  
Pred. No.: 0.0842  
Score: 10.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 3.69%  
DB: 3  
Gaps: 0

US-09-806-277a-6 (1-271) x US-08-787-739-32 (1-93)

QY 53 G1YAlaProG1yArProG1yArGyAlaGly 62  
Db 51 GGGGGCCCCGGAGGCGCTGGCGGTGTGC 80

RESULT 7  
US-08-487-077A-32  
Sequence 32, Application US/08487077A  
Patent No. 60693242  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,077A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-487-077A-32

Alignment Scores:  
Pred. No.: 0.0842  
Score: 10.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 3.69%  
DB: 3  
Gaps: 0

US-09-806-277a-6 (1-271) x US-08-487-077A-32 (1-93)

QY 53 G1YAlaProG1yArProG1yArGyAlaGly 62  
Db 51 GGGGGCCCCGGAGGCGCTGGCGGTGTGC 80

RESULT 8  
US-08-485-863A-32  
Sequence 32, Application US/08485863A  
Patent No. 6093548  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,863A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:



LENGTH: 93 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 DESCRIPTION: 5th MN exon  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-485-863A-32

Alignment Scores:  
 Pred. No.: 0.0842 Length: 93  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.69% Indels: 0  
 DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-485-863A-32 (1-93)

OY 53 G1YAlAPrOgIYArgPrOgIYArgVA1G1Y 62  
 Db 51 GGGGGCCCCGGAGGCTGTGCGTGTGCG 80

RESULT 9  
 US-08-485-049D-32.

Sequence 32, Application US/08485049D

Patent No. 6204370

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 369 Pine Street

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,049D

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3E

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034

TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 93 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: 5th MN exon

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-485-049D-32

Alignment Scores:

Pred. No.: 0.0842 Length: 93  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.69% Indels: 0  
 DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-485-049D-32 (1-93)

OY 53 G1YAlAPrOgIYArgPrOgIYArgVA1G1Y 62  
 Db 51 GGGGGCCCCGGAGGCTGTGCGTGTGCG 80

RESULT 10  
 US-09-178-115-32

Sequence 32, Application US/09178115

Patent No. 6297041

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

TITLE OF INVENTION: MN Gene and Protein

FILE REFERENCE: D-0021.5A

CURRENT APPLICATION NUMBER: US/09/178,115

EARLIER FILING DATE: 1998-10-23

EARLIER FILING DATE: 1998-10-23

EARLIER FILING DATE: 1998-10-23

EARLIER FILING DATE: 1997-01-24

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

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EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

QY 53 G1YAlaProG1YArGProG1YArGValG1Y 62  
Db 51 GGGGGCCCCGGAGGCGCTGGCGCTGTGGC 80

## RESULT 11

US-09-177-776-32  
Sequence 32, Application US/09177776A  
Patent No. 6297051  
GENERAL INFORMATION:  
APPLICANT: Pastorek, Jaromir  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
FILE REFERENCE: D-0021.5A  
CURRENT APPLICATION NUMBER: US/09/177,776A  
EARLIER FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: 08/787,739  
EARLIER FILING DATE: 1997-01-24  
EARLIER APPLICATION NUMBER: 08/485,049  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/486,756  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/477,504  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/481,658  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,862  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,863  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/487,077  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/260,190  
EARLIER FILING DATE: 1994-06-15  
EARLIER APPLICATION NUMBER: 08/177,093  
EARLIER FILING DATE: 1993-12-30  
EARLIER APPLICATION NUMBER: 07/964,589  
EARLIER FILING DATE: 1992-10-21  
EARLIER APPLICATION NUMBER: PV-709-92  
EARLIER FILING DATE: 1992-03-11  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 93  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1)  
OTHER INFORMATION: 5th MN exon  
US-09-177-776-32

## Alignment Scores:

Pred. No.:	0.0842	Length:	93
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.69%	Indels:	0
DB:	3	Gaps:	0

US-09-806-277A-6 (1-271) x US-09-177-776-32 (1-93)

QY 53 G1YAlaProG1YArGProG1YArGValG1Y 62  
Db 51 GGGGGCCCCGGAGGCGCTGGCGCTGTGGC 80

## RESULT 12

US-09-772-719B-32  
Sequence 32, Application US/09772719B  
Patent No. 6770438  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorek, Jaromir

Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Leona L. Lauder  
STREET: 465 California Street, Suite 450  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/772,719B  
FILING DATE: 30-Jan-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,049  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3A-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332

## INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5th MN exon  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-09-772-719B-32  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:

## Alignment Scores:

Pred. No.:	0.0842	Length:	93
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.69%	Indels:	0
DB:	4	Gaps:	0

US-09-806-277A-6 (1-271) x US-09-772-719B-32 (1-93)

QY 53 G1YAlaProG1YArGProG1YArGValG1Y 62  
Db 51 GGGGGCCCCGGAGGCGCTGGCGCTGTGGC 80

## RESULT 13

US-07-964-589-1  
Sequence 1, Application US/07964589  
Patent No. 5387676  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorek, Jaromir  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Leona L. Lauder  
STREET: Steuart Street Tower, 18th Fl., One Market  
STREET: Plaza  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/964,589  
FILING DATE: 19921021  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-777-9257  
TELEFAX: 415-543-4219  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1397 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1287  
US-07-964-589-1

Alignment Scores:  
Pred. No.: 1.18 Length: 1397  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 1 Gaps: 0

US-09-806-277A-6 (1-271) x US-07-964-589-1 (1-1397)

Qy 53 G1YAlAPrOgIYAqPrOgIYAqVAlG1Y 62  
Db 684 GGGGGCCCCGGAGGCGCTGGCCGTTGGC 713

RESULT 14  
PCT-US93-02024-1  
Sequence 1, Application PC/TUS9302024  
GENERAL INFORMATION:  
APPLICANT: CIBA Corning Diagnostics Corp.  
APPLICANT: Institute of Virology  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: Stewart Street Tower, 18th Fl., One Market  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02024  
FILING DATE: 19930308  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CS PV-709-92  
FILING DATE: 10-MAR-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/964,589  
FILING DATE: 21-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-777-9257  
TELEFAX: 415-543-4219  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1397 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1287  
PCT-US93-02024-1

Alignment Scores:  
Pred. No.: 1.18 Length: 1397  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 5 Gaps: 0

US-09-806-277A-6 (1-271) x PCT-US93-02024-1 (1-1397)

Qy 53 G1YAlAPrOgIYAqPrOgIYAqVAlG1Y 62  
Db 684 GGGGGCCCCGGAGGCGCTGGCCGTTGGC 713

RESULT 15  
US-08-335-469-1  
Sequence 1, Application US/08335469A  
Patent No. 6004535  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide  
FILE REFERENCE: D-0021A  
CURRENT APPLICATION NUMBER: US/08/335,469A  
CURRENT FILING DATE: 1994-11-07  
EARLIER APPLICATION NUMBER: 07/964,589  
EARLIER FILING DATE: 1992-10-21  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1399  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1266)  
US-08-335-469-1

Alignment Scores:  
Pred. No.: 1.18 Length: 1399  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.69% Indels: 0  
DB: 3 Gaps: 0

US-09-806-277A-6 (1-271) x US-08-335-469-1 (1-1399)

Mon Dec 20 08:22:13 2004

us-09-806-277a-6.Oligo.rn1

**Page 8**

Oy 53 GLYALPRGGLYARGPRGGLYARGVALGLY 62  
 |||||  
 Db 687 GGGGCGCCGGAGGCGCTGGCCGTTGTCG 716

Search completed: December 17, 2004, 14:21:42  
Job time : 104 secs







PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 05-JUN-1998; 98US-0088126P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 09-JUN-1998; 98US-0088555P.  
PR 10-JUN-1998; 98US-0088622P.  
PR 10-JUN-1998; 98US-0088730P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.  
PR 11-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088863P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089090P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089533P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 19-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 23-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
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PR 24-JUN-1998; 98US-0090538P.  
PR 24-JUN-1998; 98US-0090539P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090691P.  
PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.

PR 01-JUL-1998; 98US-0091358P.  
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PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091486P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
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PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097951P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.

XX (GETH ) GENENTECH INC.

XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,  
PI Wood WI, Yuan J;

XX WPI; 2000-072883/06.  
XX P-FSDB; AAY6738.

XX Membrane-bound proteins and related nucleotide sequences.  
XX Claim 2; Fig 251; 822pp; English.  
PS





PI Metanabe CK, Wood WI;  
 XX WPI, 2000-572270/53.  
 DR P-PSDB; AAB24075.  
 XX

PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 PT treatment, diagnosis and prevention of cancer.  
 XX

PS Claim 50; Fig 37; 286pp; English.  
 XX

CC The present invention describes an isolated antibody that binds to one of  
 CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, PRO619,  
 CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1009, PRO1025,  
 CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,  
 CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR  
 CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The  
 CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis  
 CC and prevention of cancer. The antibodies and other anti-tumour compounds  
 CC maybe used to treat various conditions, including those characterised by  
 CC overexpression and/or activation of the amplified PRO genes. Exemplary  
 CC conditions or disorders to be treated with such antibodies and other  
 CC compounds include benign or malignant tumours (e.g., renal, liver,  
 CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,  
 CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,  
 CC glioblastomas, and various head and neck tumours), leukaemias and  
 CC lymphoid malignancies, other disorders such as neuronal, glial,  
 CC astrocytal, hypochalamic and other glandular, macrophagal, epithelial,  
 CC stromal, and blastocoele disorders, and inflammatory, angiogenic and  
 CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and  
 CC hybridisation probes used in the isolation of the human PRO sequences.  
 CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO  
 CC polynucleotide and protein sequences given in the exemplification of the  
 CC present invention  
 XX

XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;

XX Query Match 98.2%; Score 1230; DB 3; Length 1238;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GCGAGCGGAGGAGCGCCCGCTTGGCTTACGCGGTCTCAGAGATTGTCCTGCTGCG 83  
 DB 1 GCGAGCGGAGGAGCGCCCGCTTGGCTTACGCGGTCTCAGAGATTGTCCTGCTGCG 60  
 QY 84 CTCAGGATGAGGGGAGATCTGGCCCTGTGGGCGTTCTTATCAGGCTGAGCTTCTGCA 143  
 DB 61 CTCAGGATGAGGGGAGATCTGGCCCTGTGGGCGTTCTTATCAGGCTTCTGCA 120  
 QY 144 CTGCTGCTATGAGCATCTCAGCGGCTGCGATGACGCTGCTGTGCAATCTCTC 203  
 DB 121 CTGCTGCTATGAGCATCTCAGCGGCTGCGATGACGCTGCTGTGCAATCTCTC 180  
 QY 204 GTCCCTGGCTTCAAAAGGGGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGCT 263  
 DB 181 GTCCCTGGCTTCAAAAGGGGATGCGGAGAGAAAGGAGCAAAAGGCGCCCGGAGCGCT 240  
 QY 264 GGAAGAGTCGAGCCCGGAGGAGAAAGGAGCATGGGGAGCAAAAGGAGCAGAAAGGAGCT 323  
 DB 241 GGAAGAGTCGAGCCCGGAGGAGAAAGGAGCATGGGGAGCAAAAGGAGCAGAAAGGAGCT 300  
 QY 324 GTGGGTCTCATGAAAAATTGGTCCATTGGCTTAAAGGTGAGAAAGGAGATTCCGGT 383  
 DB 301 GTGGGTCTCATGAAAAATTGGTCCATTGGCTTAAAGGTGAGAAAGGAGATTCCGGT 360  
 QY 384 GACATGAGACCCCTGCTGCTTAAATGAGAAACAGGCTTCCATGTGATGACGCTAGCTG 443  
 DB 361 GACATGAGACCCCTGCTGCTTAAATGAGAAACAGGCTTCCATGTGATGACGCTAGCTG 420  
 QY 444 CGCAAGGCGCATGGGAGATGAGCAACAGGCTCTCAGCTGACGAGGAGCTCAAGTTTC 503  
 DB 421 CGCAAGGCGCATGGGAGATGAGCAACAGGCTCTCAGCTGACGAGGAGCTCAAGTTTC 480  
 QY 504 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGCAAGATCTACTGCTGTGAAG 563

DB 481 ATCAAGAAATGCTGTGCGCGGTGTGCGAGAGAGAGAGCAAGATCTACTGCTGTGAAG 540  
 QY 564 GAGAGAAAGGCTATCGGAGCGGAGCGCCAGCTGTCTTGGCAGAGCCCGGGGAGCAGCTGAGC 623  
 DB 541 GAGAGAAAGGCTATCGGAGCGGAGCGCCAGCTGTCTTGGCAGAGCCCGGGGAGCAGCTGAGC 600  
 QY 624 ATGCCAAGAGAGAGGCTGCAATGAGCTGATGAGCGCATACCTGAGCGCAGCGGCTG 683  
 DB 601 ATGCCAAGAGAGAGGCTGCAATGAGCTGATGAGCGCATACCTGAGCGCAGCGGCTG 660  
 QY 684 GCCGTGTCTTCAATCGGATCAACGACTGAGAGAGAGGCGCCCTTCTGTACTTGAC 743  
 DB 661 GCCGTGTCTTCAATCGGATCAACGACTGAGAGAGAGGCGCCCTTCTGTACTTGAC 720  
 QY 744 CATCTCCCATGAGGAGCTTCAACAGTGGCGAGCGGTGAGCCCAATGCTGTAGAC 803  
 DB 721 CATCTCCCATGAGGAGCTTCAACAGTGGCGAGCGGTGAGCCCAATGCTGTAGAC 780  
 QY 804 GAGAGAGCTGCGTGAATGAGTGTGCGCTCGGCGGCTGAGACAGCTGAGCTGACACC 863  
 DB 781 GAGAGAGCTGCGTGAATGAGTGTGCGCTCGGCGGCTGAGACAGCTGAGCTGACACC 840  
 QY 864 ACCATGACTTCAATGTGTGAGTTGACACAGAGAAATGTGAGCTTCTGAGCTGAGCTG 923  
 DB 841 ACCATGACTTCAATGTGTGAGTTGACACAGAGAAATGTGAGCTTCTGAGCTGAGCTG 900  
 QY 924 CCATTGGGGGCCCCACATGTGCTTCCGAGGGGTGGGAGGAGAGCCAGACCATGCTG 983  
 DB 901 CCATTGGGGGCCCCACATGTGCTTCCGAGGGGTGGGAGGAGAGCCAGACCATGCTG 960  
 QY 984 CAGCAGAGAGCTGTCCCTCTGTGAAGAGGTGAGAGCTCACTGATGAGAGGCTGTGTCT 1043  
 DB 961 CAGCAGAGAGCTGTCCCTCTGTGAAGAGGTGAGAGCTCACTGATGAGAGGCTGTGTCT 1020  
 QY 1044 AAATGAGAAATGTGCTTATGAGAGAAATGAAAGTGTCTGAGGCTGTGTCTC 1103  
 DB 1021 AAATGAGAAATGTGCTTATGAGAGAAATGAAAGTGTCTGAGGCTGTGTCTC 1080  
 QY 1104 TGAAGAGAGAGGTTTCAATTAAGCTGTATGTAGGCCCAATGTATTAATTAATACC 1163  
 DB 1081 TGAAGAGAGAGGTTTCAATTAAGCTGTATGTAGGCCCAATGTATTAATTAATACC 1140  
 QY 1164 CAGATATGCTTCTTCAATTAAGCTGTGTGCTTGTCCAGCTATTAATTAATCTTTAAG 1223  
 DB 1141 CAGATATGCTTCTTCAATTAAGCTGTGTGCTTGTCCAGCTATTAATTAATCTTTAAG 1200  
 QY 1224 TAGTGCAGTATGTTAATGTCAAAAAAA 1253  
 DB 1201 TAGTGCAGTATGTTAATGTCAAAAAAA 1230

RESULT 5  
 AAF4230  
 ID AAF4230 standard; cDNA; 1238 BP.  
 XX  
 AC AAF4230;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1182 (UNQ596) nucleotide sequence SEQ ID NO:356.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; cytosolic; cell death;  
 KW cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 MO200073454-A1.  
 XX  
 FN 07-DEC-2000.  
 PD  
 XX 30-MAR-2000; 2000MO-UB008439.  
 XX

XX	02-JUN-1999;	99WO-US012252.			
PR	23-JUN-1999;	99US-01410376.			
PR	07-JUL-1999;	99US-01430486.			
PR	20-JUL-1999;	99US-0144758P.			
PR	26-JUL-1999;	99US-0145698P.			
PR	28-JUL-1999;	99US-0146222P.			
PR	17-AUG-1999;	99US-0149396P.			
PR	15-SEP-1999;	99WO-US021090.			
PR	15-SEP-1999;	99WO-US021547.			
PR	08-OCT-1999;	99US-0158663P.			
PR	30-NOV-1999;	99WO-US028330.			
PR	01-DEC-1999;	99WO-US028301.			
PR	16-DEC-1999;	99WO-US030095.			
PR	20-DEC-1999;	99WO-US030911.			
PR	05-JAN-2000;	2000WO-US000219.			
PR	06-JAN-2000;	2000WO-US000376.			
PR	11-FEB-2000;	2000WO-US003565.			
PR	18-FEB-2000;	2000WO-US004341.			
PR	22-FEB-2000;	2000WO-US004414.			
PR	24-FEB-2000;	2000WO-US004914.			
PR	24-FEB-2000;	2000WO-US005004.			
PR	02-MAR-2000;	2000WO-US005841.			
PR	15-MAR-2000;	2000WO-US006884.			
PR	20-MAR-2000;	2000WO-US007377.			
XX	(GETH ) GENENTECH INC.				
PA					
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;				
PI	Ferrara N, Fong S, Gerber H, Gertlesen ME, Goddard A, Godowski PJ;				
PI	Grimaldi CJ, Gurney AL, Kijavrin IU, Napier MA, Pan J, Peoni NF;				
PI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;				
XX	Zhang Z;				
XX					
DR	WPI; 2001-032160/04.				
DR	P-PSDB; AAB65261.				
PT	PRO polynucleotides used to produce polypeptides used to target bioactive				
PT	molecules such as toxins, radiolabels or antibodies, to specific cells,				
PT	to cause targeted cell death.				
XX					
PS	Claim 2; Fig 251; 935pp; English.				
XX					
CC	The present invention describes human secreted and transmembrane PRO				
CC	proteins. The PRO proteins have cytosolic activity. The PRO proteins can				
CC	be used for targeted delivery of bioactive molecules, such as toxins,				
CC	radiolabels or antibodies, that cause cell death. PRO nucleotide				
CC	sequences, and their fragments, can be used as hybridisation probes, in				
CC	chromosomal and gene mapping, and in the generation of anti-sense RNA and				
CC	DNA. They may also be used to produce transgenic animals which are used				
CC	to develop and screen therapeutically useful reagents. The PRO nucleotide				
CC	and protein sequence can be used for tissue typing and in treating				
CC	cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to				
CC	AAF44470 represent PCR primers and hybridisation probes used in the				
CC	isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to				
CC	AAB65300 represent human PRO polynucleotide and protein sequences given				
CC	in the exemplification of the present invention				
XX					
XX					
60	Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;				
	Query Match	98.2%;	Score 1230; DB 5; Length 1238;		
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1230; Conservative	0;	Mismatches 0; Indels 0; Gaps 0		
QY	24 GGGAGCGGGAGAGACGCCCCGCTTGCTACCGCGTGTCTCAGAGATTGGTGTCTGCTGGG	83			
DB	1 GGGAGCGGGAGAGACGCCCCGCTTGCTACCGCGTGTCTCAGAGATTGGTGTCTGCTGGG	60			
QY	84 CTCAGAGATGAGGGGGAATCTGGGCCCTGTGGGGCGTTCTATCAGACCTGGACCTTCTCTGTCA	143			
DB	61 CTCAGAGATGAGGGGGAATCTGGGCCCTGTGGGGCGTTCTATCAGACCTGGACCTTCTCTGTCA	120			
QY	144 CTGCTGCATCTGAGCATCTCTCAGCCGGCTGGCGATGAGCGCTGCTCTGTGAGATCTTC	203			

Db	121	CTGCTGCCATCTGGACATCTCTAGCCGGCTGGCGATGACGCTGCTGTGTGCAGATCTTC	180
Qy	204	GTCCCTGGCCTCTCAAGGGGATGCGGGAGAAAGGAGCAAAAGCGCCCTCCGGACGGCCT	263
Db	181	GTCCCTGGCCTCAAGGGGATGCGGGAGAAAGGAGCAAAAGCGCCCTCCGGACGGCCT	240
Qy	264	GGAAGAGTGGGCCCCACGGGAGAAAAAGGAGCATGTGGGGACAAAGGACAAAGAGGCAGT	323
Db	241	GGAAAGTCGGGCCACGGGAGAAAAAGGAGCATGTGGGGACAAAGGACAAAGAGGCAGT	300
Qy	324	GTGGGTGCGTCAATGGAAAAATTTGGTCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	383
Db	301	GTGGGTGCGTCAATGGAAAAATTTGGTCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy	384	GACATAGGACCCCTGTGTCTTAATGAGAAACGAGGCTTCCATGTGAGTGACAGCCAGCTG	443
Db	361	GACATAGGACCCCTGTGTCTTAATGAGAAACGAGGCTTCCATGTGAGTGAGCCAGCTG	420
Qy	444	CGCAAGGCCATTCGGGGAGATGAGCAACGAGTCTCTCAGCTGACCAAGCCAGCTCAAGTTTC	503
Db	421	CGCAAGGCCATTCGGGGAGATGAGCAACGAGTCTCTCAGCTGACCAAGCCAGCTCAAGTTTC	480
Qy	504	ATCAAGAAATCGTGTGCGCGGTGTGGCGGAGAGGAGGAATCAACCTGCTGTGGTGAAG	563
Db	481	ATCAAGAAATCGTGTGCGCGGTGTGGCGGAGAGGAGGAATCAACCTGCTGTGGTGAAG	540
Qy	564	GAGAGAAAGCGCTGACGCGACGCCAGCTGTCTTGACAGAGGCGCGCGGGGGCAACGTGAGC	623
Db	541	GAGAGAAAGCGCTGACGCGACGCCAGCTGTCTTGACAGAGGCGCGCGGGGGCAACGTGAGC	600
Qy	624	ATGCCCAAGAGAGAGGCTTCCATAGGCTGTGATGCCCGCATTCCTGTGGCGCAAGCGGCTTG	683
Db	601	ATGCCCAAGAGAGAGGCTTCCATAGGCTGTGATGCCCGCATTCCTGTGGCGCAAGCGGCTTG	660
Qy	684	GCCCCGTGCTTCATATGGCATTCACGACCTTGAGAAAGGAGGGGCGCTTTCGTATCTGTGAC	743
Db	661	GCCCCGTGCTTCATATGGCATTCACGACCTTGAGAAAGGAGGGGCGCTTTCGTATCTGTGAC	720
Qy	744	CACCTCCCGCATGCGGACCTTCAACAAGTGGCCAGCGGTGAGACCCCAACATGCGCTACGAC	803
Db	721	CACCTCCCGCATGCGGACCTTCAACAAGTGGCCAGCGGTGAGACCCCAACATGCGCTACGAC	780
Qy	804	GAGAGAGACTGTGGGAGATGGTGGCCTTCGGCGGCTGGAACGACGCTGGCTTGCAACC	863
Db	781	GAGAGAGACTGTGGGAGATGGTGGCCTTCGGCGGCTGGAACGACGCTGGCTTGCAACC	840
Qy	864	ACCATGTACTTATGTGTGAGTTTGACAAAGAGACATGTGAGCTCAGGCTTGGGGCTGC	923
Db	841	ACCATGTACTTATGTGTGAGTTTGACAAAGAGACATGTGAGCTCAGGCTTGGGGCTGC	900
Qy	924	CCATTGGGGGGCCCAATGTCCCTGAGGGGTTGGACGGGACAGAGCCCAAGCATATGCTGC	983
Db	901	CCATTGGGGGGCCCAATGTCCCTGAGGGGTTGGACGGGACAGAGCCCAAGCATATGCTGC	960
Qy	984	CAGCCAGGGAGCTGTCCCTCTGTGAAAGGGTGGAGGCTCACTGAGTAGAGGCGCTGTGTCT	1044
Db	961	CAGCCAGGGAGCTGTCCCTCTGTGAAAGGGTGGAGGCTCACTGAGTAGAGGCGCTGTGTCT	1022
Qy	1044	AAACTGAGAAAAATGGCCTTATGCTTAAAGAGAAAAATGAAGTGTTCCTGGGGTGTCTCTC	1104
Db	1021	AAACTGAGAAAAATGGCCTTATGCTTAAAGAGAAAAATGAAGTGTTCCTGGGGTGTCTCTC	1082
Qy	1104	TGAAGAAGAGATTCACTTACTGATTTGTAAGCCCAATGTCACTATATGATTAATTAAC	1166
Db	1081	TGAAGAAGAGATTCACTTACTGATTTGTAAGCCCAATGTCACTATATGATTAATTAAC	1144
Qy	1164	CAGAAATGCTCTTCCATAAAGCTTGTGCTTGTCCAAAGCTATACATAAATCTTTAAG	1222
Db	1141	CAGAAATGCTCTTCCATAAAGCTTGTGCTTGTGTCCAAAGCTATACATAAATCTTTAAG	1200
Qy	1224	TATGTCAAGTAAATGTTCAAAAAA	1253

Db	1201	TAGTGCA	GTAGT	TAAGTC	CAAAAAA	AAAAA	1230
RESULT 6							
ABL88155							
ID	ABL88155	standard;	cdna;	1238	BP.		
XX	AC						
XX	ABL88155;						
XX	DT	16-MAY-2002	(first entry)				
XX	DE	Human PRO1182	cdna sequence SEQ ID NO:167.				
XX	Human	angio genesis;	cardiant;	cyto static;	anti angiogenic;	hypotensive;	
XX	Human	vulnery;	antiarterio sclerotic;	PRO agonist;	PRO antagonist;	trauma;	
XX	Human	gene therapy;	cardiovascular disorder;	endothelial disorder;	cancer;		
XX	Human	angiogenic disorder;	cardiac hypertrophy;	atherosclerosis;	hypertension;		
XX	Human	age-related macular degeneration;	arterial restenosis;	angina;			
XX	Human	rheumatoid arthritis;	myocardial infarction;	chromophlebitis;			
XX	Human	lymphangitis;	tumour angiogenesis;	breast carcinoma;	liver carcinoma;		
XX	Human	wound healing;	chromosome mapping;	gene mapping;	gene;	ss.	
XX	OS	Homo sapiens.					
XX	PN	WO200200690-A2.					
XX	PD	03-JAN-2002.					
XX	PF	20-JUN-2001;	2001WO-US019692.				
XX	PR	23-JUN-2000;	2000US-0233637P.				
XX	PR	20-JUL-2000;	2000US-0219586P.				
XX	PR	25-JUL-2000;	2000US-0220624P.				
XX	PR	25-JUL-2000;	2000US-0220664P.				
XX	PR	28-JUL-2000;	2000WO-US020710.				
XX	PR	02-AUG-2000;	2000US-0222695P.				
XX	PR	17-AUG-2000;	2000US-00643657.				
XX	PR	23-AUG-2000;	2000WO-US023522.				
XX	PR	24-AUG-2000;	2000WO-US023328.				
XX	PR	07-SEP-2000;	2000US-0230978P.				
XX	PR	18-SEP-2000;	2000US-00664610.				
XX	PR	18-SEP-2000;	2000US-00665350.				
XX	PR	24-OCT-2000;	2000US-0249292P.				
XX	PR	08-NOV-2000;	2000US-0070923P.				
XX	PR	08-NOV-2000;	2000WO-US030952.				
XX	PR	10-NOV-2000;	2000WO-US030873.				
XX	PR	01-DEC-2000;	2000WO-US032678.				
XX	PR	20-DEC-2000;	2000US-00747259.				
XX	PR	20-DEC-2000;	2000WO-US034956.				
XX	PR	22-JAN-2001;	2001US-00767609.				
XX	PR	28-FEB-2001;	2001US-00766498.				
XX	PR	28-FEB-2001;	2001WO-US006520.				
XX	PR	01-MAR-2001;	2001WO-US006656.				
XX	PR	09-MAR-2001;	2001US-00802706.				
XX	PR	14-MAR-2001;	2001US-00808689.				
XX	PR	22-MAR-2001;	2001US-00816744.				
XX	PR	05-APR-2001;	2001US-00828356.				
XX	PR	10-MAY-2001;	2001US-00854208.				
XX	PR	10-MAY-2001;	2001US-00854280.				
XX	PR	25-MAY-2001;	2001US-00866028.				
XX	PR	25-MAY-2001;	2001US-00866034.				
XX	PR	25-MAY-2001;	2001WO-US017092.				
XX	PR	30-MAY-2001;	2001US-00870574.				
XX	PR	30-MAY-2001;	2001WO-US017443.				
XX	PR	01-JUN-2001;	2001WO-US017800.				
XX	PA	(GETH ) GENENTECH INC.					
XX	PI	Baker KP, Ferrara N, Gerber H, Gertlesen ME, Goddard A;					
XX	PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,					
XX	PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;					
XX	DR	WPI; 2002-090516/12.					

DR	P-PSDB;ABB84900.
XX	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PR	infarction), endothelial or angiogenic disorders in a mammal.
XX	
PS	Claim 2; Fig 167; 565pp; English.
XX	
CC	ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC	ABB85003. The PRO proteins and polynucleotides have cardiant, cytoelastic,
CC	antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC	activities, and can be used in gene therapy. The PRO polynucleotides,
CC	proteins, agonists and antagonists are useful for treating or diagnosing
CC	a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC	cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC	atherosclerosis, hypertension, arterial reestenosis, rheumatoid arthritis,
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC	healing. The PRO polynucleotides have applications in molecular biology,
CC	including use as hybridisation probes, and in chromosome and gene
CC	mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX	exemplification of the present invention
SQ	
	Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
Query Match	98.2%; Score 1230; DB 6; Length 1238;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1230; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Oy	24 GCGACGGGACAGACGCCCCGTTCGCTCAGCCGCTGCATGAGGTTGTCTCTGCTGCG 83
Db	1 GCGACGGGCAAGAACGCCCGTTCGCTCAGCGGTGCTCAGGAGTTGTCTCTGCTGCG 60
Oy	84 CTGAGGATGAGGGGGGAATCTGGCCCTTGTTGGGCGTTCTAATCAGCCTTGCCCTTCTGCA 143
Db	61 CTCAGAGTAGAGGGGGAAATCTGGCCCTTGTTGGGCGTTCTAATCAGCCTTGCCCTTCTGTA 120
Oy	144 CTGCTGCATCTGGACATCTCAGCCGGCTGGCGATGACGCGCTGCTCTGTGACAGATTCTC 203
Db	121 CTGCTGCCATCTGGACATCTCAGCCGGCTGGCATGACGCTGCTGTGTGACAGATTCTC 180
Oy	204 GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGCAAAAGCGCCCCCGAGCGGCTT 263
Db	181 GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGCAAAAGCGCCCCCGAGCGGCTT 240
Oy	264 GGAAAGTTCGGCCCAACGGGAGAAAAGAGACATGGGGGACAAGAGACAGAAAGGACGT 323
Db	241 GGAAAGTTCGGCCCAACGGGAGAAAAGAGACATGGGGGACAAGAGACAGAAAGGACGT 300
Oy	324 GTGGGTCTGTCATGGAATAATTGTCCTCATTTGGCTCTAAAGGTGAGAAAAGAGATTCCG 383
Db	301 GTGGGTCTGTCATGGAATAATTGTCCTCATTTGGCTCTAAAGGTGAGAAAAGAGATTCCG 360
Oy	384 GACATAGAACCCCCTTGTTCTTAATGGAAGAACAGGCTCCCATGTGAGTGCAGCCACTG 443
Db	361 GACATAGAACCCCCTTGTTCTTAATGGAAGAACAGGCTCCCATGTGAGTGCAGCCACTG 420
Oy	444 CGCAAGGCCATGGGGGAGATGAGCAACACAGGCTCTCAGCTGACACAGAGCTCAAGTTT 503
Db	421 CGCAAGGCCATGGGGGAGATGAGCAACACAGGCTCTCAGCTGACACAGAGCTCAAGTTT 480
Oy	504 ATCAAGATGCTGTGCGCGGTGTGCGGAGACGAGAGCAGATCTAATCTGCTGTGGAAG 563
Db	481 ATCAAGATGCTGTGCGCGGTGTGCGGAGACGAGAGCAGATCTAATCTGCTGTGGAAG 540
Oy	564 GAGGAGGAAGCGGTACGCGGAGCGCCAGCTGCTCTCAGCTGACACAGAGCTCAAGCTG 623
Db	541 GAGGAGGAAGCGGTACGCGGAGCGCCAGCTGCTCTCAGCTGACACAGAGCTCAAGCTG 600
Oy	624 ATGCCCAAGAGACGAGGCTGCTCAATGAGCTTATGAGCGCATACCTTGCGCAAGCGGCTTG 683
Db	601 ATGCCCAAGAGACGAGGCTGCTCAATGAGCTTATGAGCGCATACCTTGCGCAAGCGGCTTG 660

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QY 684 GCCCGTGTCTTCATCGGCATCAACGACCTGAGAGAGAGGCGCTTGTGACTCTGAC 743
Db 661 GCCCGTGTCTTCATCGGCATCAACGACCTGAGAGAGAGGCGCTTGTGACTCTGAC 720
QY 744 CACTCCCCCATCGGACCTTCAACAGTGGCGACGGGTGAGGCCCAACATGCTTACGAC 803
Db 721 CACTCCCCCATCGGACCTTCAACAGTGGCGACGGGTGAGGCCCAACATGCTTACGAC 780
QY 804 GAGAGGAGCTGCGTGGAGATGTTGGCTCGGGCGGCTGAAAGACAGTGGCTGCGACACC 863
Db 781 GAGAGGAGCTGCGTGGAGATGTTGGCTCGGGCGGCTGAAAGACAGTGGCTGCGACACC 840
QY 864 ACCATGTACTTCATGTGTGAGTTTGAACAAGAGACATGTGAGCTCAGAGCTGGGGCTGAC 923
Db 841 ACCATGTACTTCATGTGTGAGTTTGAACAAGAGACATGTGAGCTCAGAGCTGGGGCTGAC 900
QY 924 CCATTGGGGGGCCCCCATGTGCTCCCTGACAGGGTTGGAGGAGACAGAGCCAGACATGTGTC 983
Db 901 CCATTGGGGGGCCCCCATGTGCTCCCTGACAGGGTTGGAGGAGACAGAGCCAGACATGTGTC 960
QY 984 CAGCCAGGAGAGCTGCTCTCTGTGTGAAGGGTGGAGGCTCACTGAGTGAAGGGCTGTGTCT 1043
Db 961 CAGCCAGGAGAGCTGCTCTCTGTGTGAAGGGTGGAGGCTCACTGAGTGAAGGGCTGTGTCT 1020
QY 1044 AAACGTAGAGAAATGAGCTATGCTTAAGAGAGAAATGAAAGTGTCTGCGGGGTGCTGTCTC 1103
Db 1021 AAACGTAGAGAAATGAGCTATGCTTAAGAGAGAAATGAAAGTGTCTGCGGGGTGCTGTCTC 1080
QY 1104 TGAAGAGACAGAGTTTCACTTACTCTGATTTGTAAGCCCAATGCTATGTAATTAATTAAC 1163
Db 1081 TGAAGAGACAGAGTTTCACTTACTCTGATTTGTAAGCCCAATGCTATGTAATTAATTAAC 1140
QY 1164 CAGAACTGCTCTTCCATTAAGCTTGTGCTTGTCAAGCTTATACAAATAAATCTTTAAG 1223
Db 1141 CAGAACTGCTCTTCCATTAAGCTTGTGCTTGTCAAGCTTATACAAATAAATCTTTAAG 1200
QY 1224 TAGTCAGTACTTAAGTCCAAAAAATAAATA 1253
Db 1201 TAGTCAGTACTTAAGTCCAAAAAATAAATA 1230

RESULT 7
ABL95644
ID ABL95644 standard; cDNA; 1238 BP.
AC ABL95644;
XX
XX
XX 19-JUL-2002 (first entry)
DT
XX
XX Human anglogenesis related cDNA P101182 SEQ ID NO: 167.
DE
XX
XX Human; anglogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; se.
XX
OS Homo sapiens.
XX
XX WO200208284-A2.
PN
XX
XX 31-JAN-2002.
PD
XX
XX 09-JUL-2001; 2001WO-US02175.
XX
XX 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
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PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-07109238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
XX (GETH ) GENENTECH INC.
PA (BAKE ) BAKER K P.
PA (FERR ) FERRARA N.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (MARS ) MARSTERS S A.
PA (PANU ) PAN J.
PA (PAON ) PAONTI N F.
PA (STEP ) STEPHAN J F.
PA (WATA ) WATANABE C K.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AJ, Hillan KJ, Marsters SA, Pan J,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX WPI, 2002-171999/22.
DR P-PSDB; ABB95506.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PR useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 1; Fig 167; 567pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;
SQ
XX
XX Query Match 98.2%; Score 1230; DB 6; Length 1238;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 24 GCGAGGCGCAGAGCGCCCGCTTCCGCTTACGCGGCTCAGAGAGTTGCTGTCTGCTGCGG 83

Db 1 GCGAGGGGACAGAGCCCGTTCCGCTAGCGGTCTCAGAGAGTTGGTCTGCTGCTGCG 60  
Qy 84 CTCAGAGATGAGGGGAAATCTGGCCCTGGTGGCGCTTCTTAATCAGCTGGCTTCTCTCA 143  
Db 61 CTCAGAGATGAGGGGAAATCTGGCCCTGGTGGCGCTTCTTAATCAGCTGGCTTCTCTCA 120  
Qy 144 CTGCTGCCATCTGAGCATCTCAGCGGGCTGGCGATGAGCGCTGTCTGTGCAGATCTCTC 203  
Db 121 CTGCTGCCATCTGAGCATCTCAGCGGGCTGGCGATGAGCGCTGTCTGTGCAGATCTCTC 180  
Qy 204 GTCCCTGGCTCAAGGGGATGCGGAGAGAGGAGCAAAAGCGCCCGGACGCGCT 263  
Db 181 GTCCCTGGCTCAAGGGGATGCGGAGAGAGGAGCAAAAGCGCCCGGACGCGCT 240  
Qy 264 GGAAGAGTGGGCCCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
Db 241 GGAAGAGTGGGCCCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
Qy 324 GTGGGTCTCATGAG 383  
Db 301 GTGGGTCTCATGAG 360  
Qy 384 GACATAG 443  
Db 361 GACATAG 420  
Qy 444 CGCAGAGGCTATCGGAG 503  
Db 421 CGCAGAGGCTATCGGAG 480  
Qy 504 ATCAAGAGATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 563  
Db 481 ATCAAGAGATGCTGTGCGCGGTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Qy 564 GAGAGAGAGCGCTACGCGGAGCGCCAGCTGTCTGCGAGGGCGCGGGGAGCAGCTGAG 623  
Db 541 GAGAGAGAGCGCTACGCGGAGCGCCAGCTGTCTGCGAGGGCGCGGGGAGCAGCTGAG 600  
Qy 624 ATGCGCCAAAG 683  
Db 601 ATGCGCCAAAG 660  
Qy 684 GCCCGTGTCTCATCGGAG 743  
Db 661 GCCCGTGTCTCATCGGAG 720  
Qy 744 CACTCCCCATGCGGAG 803  
Db 721 CACTCCCCATGCGGAG 780  
Qy 804 GAGAGAGAGCTGCGGAG 863  
Db 781 GAGAGAGAGCTGCGGAG 840  
Qy 864 ACCATGATCTCATGTGTGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923  
Db 841 ACCATGATCTCATGTGTGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
Qy 924 CCATTGGGGGCCCCCAATGTCCTGCGAGGGTTGGCAGGGAGCAGAGCCAGCATGTGTC 983  
Db 901 CCATTGGGGGCCCCCAATGTCCTGCGAGGGTTGGCAGGGAGCAGAGCCAGCATGTGTC 960  
Qy 984 CAGCAGAGAGAGCTGCTCCCTGTGTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043  
Db 961 CAGCAGAGAGAGCTGCTCCCTGTGTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
Qy 1044 AAATCTGAGAAATGAGCTATGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103  
Db 1021 AAATCTGAGAAATGAGCTATGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
Qy 1104 TGAAG 1163

Db 1081 TGAAG 1140  
Qy 1164 CAGAGATGCTCTTCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223  
Db 1141 CAGAGATGCTCTTCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
Qy 1224 TAGTCAGTGTGTTAAGTCAAAAAA 1253  
Db 1201 TAGTCAGTGTGTTAAGTCAAAAAA 1230

RESULT 8  
AC64399  
ID AC64399 standard; cDNA; 1238 bp.  
XX AC64399;  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein Prol182 cDNA.  
XX  
KW Human; secreted and transmembrane protein; cytoprotective; anti-HIV;  
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;  
KW PRO; pharmaceutical; diagnostic; biosensor; bioindicator; malignancy;  
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; Leukemia;  
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;  
KW drug screening; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US200303531-A1.  
XX  
PD 02-JAN-2003.  
XX  
PF 19-NOV-2001; 2001US-0089734.  
XX  
XX 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97MO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 05-JUN-1998; 98US-0088555P.  
PR 09-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.





Db 661 GCCCGTGTCTTCATCGCATCAACGACCTGGAGAGAGAGGCGGCTTGTGTACTGTAC 720  
Qy 744 CACTTCCCCCATGCGGACCTTCAACAATGGCGCAGCGGTGAGCCCAACAATGCTTAGAC 803  
Db 721 CACTCCCCCATGCGGACCTTCAACAATGGCGCAGCGGTGAGCCCAACAATGCTTAGAC 780  
Qy 804 GAGAGGACCTCGTGGAGATGGTGGCTCGGGCGGCTGGAACGAGTGGCTGGCACACC 863  
Db 781 GAGAGGACCTCGTGGAGATGGTGGCTCGGGCGGCTGGAACGAGTGGCTGGCACACC 840  
Qy 864 ACCATGTACTTCATGTGTGACTTTGACAAGAGAAACATGTAGGCTCAGGCTGGGGCTGC 923  
Db 841 ACCATGTACTTCATGTGTGACTTTGACAAGAGAAACATGTAGGCTCAGGCTGGGGCTGC 900  
Qy 924 CCATTGGGGGCGCCACATGTCCTCGCAGGCTTGGCAGGGAACAGGCCCAACATGTGGTC 983  
Db 901 CCATTGGGGGCGCCACATGTCCTCGCAGGCTTGGCAGGGAACAGGCCCAACATGTGGTC 960  
Qy 984 CAGCCAGGAGCTGTCCCTCTGTGAGAGGGTGGAGGCTCACTGAGTAGAGGGCTGTGTCT 1043  
Db 961 CAGCCAGGAGCTGTCCCTCTGTGAGAGGGTGGAGGCTCACTGAGTAGAGGGCTGTGTCT 1020  
Qy 1044 AAACCTGAGAAAATGCGCTTATGAGAGAGAAAATGAAAGTTCCTGGGGTGTGTCTC 1103  
Db 1021 AAACCTGAGAAAATGCGCTTATGAGAGAGAAAATGAAAGTTCCTGGGGTGTGTCTC 1080  
Qy 1104 TGAAGAAGCAGATTTCTTACCTGTATGTAGCCCAATGTCATTTATGTAATTAATACC 1163  
Db 1081 TGAAGAAGCAGATTTCTTACCTGTATGTAGCCCAATGTCATTTATGTAATTAATACC 1140  
Qy 1164 CAGATTTGCTCTTCCATTAAGCTTGTGCTTGTCCAAGCTATACAAATAAATCTTTAAG 1223  
Db 1141 CAGATTTGCTCTTCCATTAAGCTTGTGCTTGTCCAAGCTATACAAATAAATCTTTAAG 1200  
Qy 1224 TAGTGCACTAGTTAAGTCCAAAAA 1253  
Db 1201 TAGTGCACTAGTTAAGTCCAAAAA 1230

RESULT 9  
ABX80858  
ID ABX80858 standard; cDNA; 1238 BP.  
XX  
AC ABX80858;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein cDNA, #144.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioeffector; tumour; therapeutic; gene therapy;  
KW tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated produg therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-00997428.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
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OY	144	CTGCTGCCATCTGGACATCTTCAGCCGGCTTGGCGATGACGCTGTCTGTGTCAAGATCTC	203
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OY	264	GGAAGAGTGGCGCCCAACGGGAGAAAAAGAGACATGGGGGAGCAAAAGGACAGAAAGCGAGT	323
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Db	301	GTGGGTGTCATGGAAAAAATTGGTCCCATTTGGCTTAAAGGTGAGAAAGAGATTCGGT	360
OY	384	GACATAGAGACCCCTGGTCTTAATGAGAAACCAAGCTCCCATGTGTAGTCCAGCCAGCTG	443
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Db	421	CGCAAGGCCATCGGGGAGATGGAACAACAGAGTCTCAGCTGACCAAGCGAGCTCAAGTTC	480
OY	504	ATCAAGATGCTGTGCGCCGGTGTGCGGAGACGGAGACGAAGATCTTACCTTGGTGAAG	563
Db	481	ATCAAGATGCTGTGCGCCGGTGTGCGGAGACGGAGACGAAGATCTTACCTTGGTGAAG	540
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OY	624	ATGCGCAAGGACGAGCGTCGCAATAGCGCTGATGGCGCATACCTGGGCGCAAGCGCGGCTG	683
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OY	684	GCCCGTGTCTTCAATCGGCATCAACGACCTTGAGAGAGAGGCGCGCTTGTGTACTGTGAC	743

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DT 10-SEP-2003 (first entry)  
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KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
KW gene therapy; gene; ss.  
OS Homo sapiens.  
XX  
PN US2002127576-A1.  
XX  
PD 12-SEP-2002.  
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PR 16-SEP-1998; 98WO-US019330.  
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PR 05-JAN-1999; 99WO-US000106.  
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PR 15-SEP-1999; 99WO-US021090.  
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PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
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PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005941.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014942.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUN-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000MO-US030952.  
PR 01-DEC-2000; 2000MO-US032678.  
PR 28-FEB-2001; 2001MO-US006520.  
PR 01-JUN-2001; 2001MO-US017800.  
PR 20-JUN-2001; 2001MO-US019692.  
PR 29-JUN-2001; 2001MO-US021066.  
PR 09-JUL-2001; 2001MO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,  
PI Ferraraz N, Fong S, Gerber H, Gerltzen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gunney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NP,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX MPI; 2003-340824/32.  
DR P-PSDB; ABO25998.  
XX  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT and are therapeutically useful for enhancing immune responses.  
XX  
XX Claim 2; Fig 251; 661pp; English.  
XX  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC biactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for for  
CC identifying agonists or antagonists. The polynucleotide sequences  
CC encoding PRO polypeptides are useful as hybridisation probes, in  
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
CC in the preparation of PRO polypeptides, for generating transgenic animals  
CC or knockout animals, to construct hybridisation probes for mapping the  
CC gene which encodes the PRO polypeptide, and for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome  
CC identification, as chromosome markers, and for generating probes for PCR,  
CC Northern analysis, Southern analysis and Western analysis. The present  
CC sequence encodes a human PRO polypeptide of the invention. Note: The  
CC sequence data for this patent was obtained in electronic format directly  
CC from the USPTO web site at [seqdata.uspto.gov/patipdbidntry.html](http://seqdata.uspto.gov/patipdbidntry.html)  
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QY 204 GTCCCTGGCTCAAGAGGGAGTGGGAGAGAGAGCAAAAGCGCCCGCGAGCGCT 263  
DB 181 GTCCCTGGCTCAAGAGGGAGTGGGAGAGAGAGAGCAAAAGCGCCCGCGAGCGCT 240  
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KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
OS Homo sapiens.  
PN US2002142961-A1.  
XX 03-OCT-2002.  
XX 19-NOV-2001; 2001US-00989771.  
XX 16-JUN-1997; 97US-0049787P.  
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XX 16-SEP-1998; 98WO-US019330.  
XX 17-SEP-1998; 98WO-US019437.  
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XX 02-JUN-1999; 99WO-US012252.  
XX 15-SEP-1999; 99WO-US021090.  
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XX 01-DEC-1999; 99WO-US028313.  
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PR 26-AUG-2001; 2001US-00941992.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AV, Baker KP, Botstein D, Deenoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MW, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX WPI; 2003-155950/15.  
DR P-PSDB; ABUS9007.  
XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
XX Claim 2; Fig 251; 647pp; English.  
XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
CC colon, lung or breast cancer) and diagnostic determination of the  
CC presence of these cancers. The PRO polypeptides are also useful as  
CC molecular weight markers or for chromosome identification. The PRO genes  
CC are useful as hybridisation probes or for screening libraries of human  
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
CC therapy, particularly for replacing a defective gene. The sequences  
CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
CC amplifying and the probes detecting the PRO polynucleotides of the  
CC invention. Note: The sequence data for this patent is also available in  
CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX  
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 U; 0 Other;



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KW Human, PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
OS Homo sapiens.  
XX  
FN US2003027985-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 14-NOV-2001; 2001US-00990562.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
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 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088736P.  
 PR 10-JUN-1998; 98US-0088742P.  
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 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088826P.

PI Aghazeni AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gertlissen ME, Goddard A, Gadowski PJ,  
 PI Grimaldi JC, Gurney AL, Kjaava IJ, Nandier MA, Pan J,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM,  
 PI Zhang Z;  
 XX  
 WPI: 2003-066810/06.  
 DR P-PSDB: ABU109322.  
 DR

antagonists of polypeptide, and as molecular weight markers.

Claim 2, Fig 251, 655bp; English.

The invention relates to a secreted and transmembrane polypeptide, termed PRO polypeptide, and the polynucleotide encoding it. The polypeptide is useful for detecting and pro polypeptides and for linking a bioactive molecule to a cell expressing the above polypeptides, where the bioactive molecule is a toxin, radiolabel or an antibody. The bioactive material causes the death of the cell. The polypeptide is useful for identifying of agonists or antagonists of the PRO polypeptide, for preparing variants of PRO, as a molecular weight marker for protein electrophoresis purposes and the PRO polynucleotide is useful for recombinantly expressing those markers. The polynucleotide is also useful as a hybridisation probe, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes PRO and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as a chromosome marker and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. This sequence represents a human PRO polynucleotide of the invention

Sequence 1238 BP, 293 A, 321 C, 389 G, 235 T, 0 U, 0 Other;

Query Match 98.2%; Score 1230; DB 8; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 GGCATGGGCGACGAGCGCCCGCTTCCGCTTAGCCGCTGCAGAGATTGGTCCCTCCGCG 83  
1 GCGAGGGGCGACGAGCGCCCGCTTCCGCTTAGCCGCTGCAGAGATTGGTCCGCTGC 60  
84 CTGAGGATGAGAGGGGGAATCTGGCCCTGGTGGGGCTTCTTAATCAGCCTGGCTTCCTGCA 143  
61 CTCAGAGTGAAGGGGGAATCTGGCCCTGGTGGGGCTTCTTAATCAGCCTGGCTTCCTGCA 120  
144 CTGCTGCATCTGGAATCTCTAGCCGGCTGGCGATGACGCTGCTCTGTGCAATCCTC 203  
121 CTGCTGCATCTGGAATCTCTAGCCGGCTGGCGATGACGCTGCTCTGTGCAATCCTC 180  
204 GTCCTTGGCTCAAGAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
181 GTCCTTGGCTCAAGAGGGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
264 GGAAGAGTCGGCCCGCCGAG 323  
241 GGAAGAGTCGGCCCGCCGAG 300  
324 GTGGGTCTCATATGAAATAATTGGTCCATTGGCTTAAAGGTGAAGAAAGAGATTCCGGT 383  
301 GTGGGTCTCATATGAAATAATTGGTCCATTGGCTTAAAGGTGAAGAAAGAGATTCCGGT 360  
384 GACATAGAGACCCCTGTGCTTAATGAGAGACAGGCTCCCATGTGATGAGCCAGCTG 443  
361 GACATAGAGACCCCTGTGCTTAATGAGAGACAGGCTCCCATGTGATGAGCCAGCTG 420  
444 GCGAAGGCTATCGGGGAGATGAGACACAGGCTCTCAGCTGACACGAGACCTCAAGTTC 503  
421 GCGAAGGCTATCGGGGAGATGAGACACAGGCTCTCAGCTGACACGAGACCTCAAGTTC 480  
504 ATCAAGAAATGCTGTGCGCGGTGCGCAGAGACGAGAGACAAATCTACTGTGGTAG 563  
481 ATCAAGAAATGCTGTGCGCGGTGCGCAGAGACGAGAGACAAATCTACTGTGGTAG 540  
564 GAGAGAAAGCGTATCGCGAGAGCCACGCTGTCTCCACAGGGCTCGGGGGGCACTGTAGC 623  
541 GAGAGAAAGCGTATCGCGAGAGCCACGCTGTCTCCACAGGGCTCGGGGGGCACTGTAGC 600

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Db      601 ATGCCAAGAGAGAGGCTGCCAATGGCTGATGGCCGCATACCTGGCGAAGCCGGCCTG 660
QY      684 GCCCGTGTCTTCATGTGGCATCAACGACTTGGAGAGAGGGGCGCTTGTGTACTCTGAC 743
Db      661 GCCGTGTCTTCATGTGGCATCAACGACTTGGAGAGAGGGGCGCTTGTGTACTCTGAC 720
QY      744 CACTCCCCCATGGGACCTTCAACAAAGTGGCGACAGGGTGAAGCCCAACATGGCTTACGAC 803
Db      721 CACTCCCCCATGGGACCTTCAACAAAGTGGCGACAGGGTGAAGCCCAACATGGCTTACGAC 780
QY      804 GAGAGAGACTGCGTGGAGATGGTGGCTCGGGCGGCTGAAAAGACGTGGCCTGCCACACC 863
Db      781 GAGAGAGACTGCGTGGAGATGGTGGCTCGGGCGGCTGAAAAGACGTGGCCTGCCACACC 840
QY      864 ACCATGTACTTCATGTGTGAAGTTTGAACAAGAGAACATGTGAGCTCAAGGCTGGGGCTGC 923
Db      841 ACCATGTACTTCATGTGTGAAGTTTGAACAAGAGAACATGTGAGCTCAAGGCTGGGGCTGC 900
QY      924 CCATTGGGGGCCCCCATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAAGCATGTGTC 983
Db      901 CCATTGGGGGCCCCCATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAAGCATGTGTC 960
QY      984 CAGCCAGGAGCTGTCCCTGTGTGAAGGGTGAAGGCTCACTGAGTGAAGGGCTGTGTCT 1043
Db      961 CAGCCAGGAGCTGTCCCTGTGTGAAGGGTGAAGGCTCACTGAGTGAAGGGCTGTGTCT 1020
QY      1044 AAACCTGAGAAAAATGGCTTATGTGAAGGAAAAATGAAAGTGTCTCTGGGGTCTGTCTC 1103
Db      1021 AAACCTGAGAAAAATGGCTTATGTGAAGGAAAAATGAAAGTGTCTCTGGGGTCTGTCTC 1080
QY      1104 TGAAGAAAGCAGAGTTTCATTACCTGTATTTAGCCCCAATGTCAATTATTAATTATACC 1163
Db      1081 TGAAGAAAGCAGAGTTTCATTACCTGTATTTAGCCCCAATGTCAATTATTAATTATACC 1140
QY      1164 CAGAAATTGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCTATACATTAATAATCTTTAAG 1223
Db      1141 CAGAAATTGCTCTTCCATTAAGCTTGTGCTTGTCCAAAGCTATACATTAATAATCTTTAAG 1200
QY      1224 TAGTGCAGTAGTTAAGTCCAAAAAAA 1253
Db      1201 TAGTGCAGTAGTTAAGTCCAAAAAAA 1230
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Job time : 929 secs

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